

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 72.4256 Seconds

(without alignments)
4426.083 Million cell updates/sec

Title: US-10-073-064-5
Perfect score: 3338
Sequence: 1 MVVQTRPPSWIILCYIMLG.....DGMETQHNKKMIASCSRL 626

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3195	95.7	610	Q8CC52	Q8CC52 mus musculus
2	3191	95.6	998	EP47_MOUSE	Q61772 mus musculus
3	3187.5	95.5	994	Q8R3B1	Q8R3B1 mus musculus
4	3187	95.5	998	Q8BSU8	Q8BSU8 mus musculus
5	3175	95.1	998	EP47_RAT	P54759 rattus norv
6	3139	94.0	998	EP47_HUMAN	Q15375 homo sapien
7	3126	93.6	993	Q8C7N2	Q8C7N2 mus musculus
8	3031.5	90.8	993	EP47_CHICK	Q42422 gallus gall
9	1860.5	55.7	681	Q8C276	Q8C276 mus musculus
10	1819	54.5	1005	EP45_RAT	P54757 rattus norv
11	1817	54.4	1037	EP45_HUMAN	P54755 homo sapien
12	1800	53.9	1013	EP45_CHICK	P54755 gallus gall
13	1799	53.9	984	Q8BRB1	Q8BRB1 mus musculus
14	1796	53.8	983	EP43_HUMAN	P29320 homo sapien
15	1796	53.8	983	Q8C4R6	Q8C4R6 homo sapien
16	1795.5	53.8	986	EP44_XENLA	Q91845 xenopus lae
17	1795	53.8	984	Q8C3D1	Q8C3D1 mus musculus
18	1790.5	53.6	985	EP4B_XENLA	Q91694 xenopus lae
19	1789.5	53.6	986	Q7ZYMT	Q7ZYMT xenopus lae
20	1788	53.6	969	Q7Z3F2	Q7Z3F2 homo sapien
21	1787.5	53.6	984	EP43_RAT	P29318 rattus norv
22	1783.5	53.4	983	EP43_CHICK	P29318 gallus gall
23	1783.5	53.4	983	EP43_MOUSE	P29319 mus musculus
24	1782.5	52.5	986	EP44_CHICK	Q07496 gallus gall
25	1741.5	52.2	986	EP44_HUMAN	P54764 homo sapien
26	1739	52.1	938	Q8C9K6	Q8C9K6 mus musculus
27	1728	51.8	986	Q8QVZ2	Q8QVZ2 mus musculus
28	1723	51.6	986	EP44_MOUSE	Q03137 mus musculus
29	1701.5	51.0	1005	EP4B_HUMAN	P29322 homo sapien
30	1695	50.8	1004	EP4B_MOUSE	Q03127 mus musculus
31	1655	49.6	948	EP46_RAT	P54758 rattus norv

ALIGNMENTS

RESULT 1	ID	Q8CC52	PRELIMINARY;	PRT;	610 AA.
AC	Q8CC52				
DT	01-MAR-2003 (TREMBLrel. 23, Created)				
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Mus musculus adult male diencephalon cDNA, Riken full-length enriched library, clone:9330112M1 product:Eps Receptor A7, full insert sequence.				
GN	Name=Bpha7;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;				
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
RA	Carpinci P., Hayashizaki Y.;				
RT	"High-efficiency full-length cDNA cloning.";				
RL	Meth. Enzymol. 303:19-44(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;				
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;				
RA	RIKEN FANTOM Consortium;				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;				
RA	The FANTOM Consortium;				
RT	"The RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";				
RL	Nature 420:563-573(2002).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;				
RX	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;				
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,				
RT	Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;				
RL	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";				
RL	Genome Res. 10:1617-1630(2000).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;				
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;				
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,				
RT	Kono H., Akiyama U., Nishi K., Kitounai T., Tashiro H., Itoh M.,				
RL	Sun N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,				
RL	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,				

RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Murakami M., Inoue Y., Kira A., Hayashizaki Y.;
RT "MIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN 161
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RA Aachai J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Hayashida K., Furuta M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kacoh H., Kawai J., Kojima Y., Kondo S., Komoto H., Kouda M., Koya S.,
RA Kuchihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Sakita H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Yamamatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK033903; BAC28509.1; -
DR HSSP; P54763; INUK.
DR MGD; MGI:95276; Epha7.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001090; Ephrin_receptor.
DR InterPro; IPR003962; Fcrl1 subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR008979; Gal_bind like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR001426; Ykase_receptor.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; Fn3; 1.
DR PRINTS; PR00014; FMYPEIII.
DR PRODOM; PD001495; Ephrin_receptor; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
KW Receptor.
SQ SEQUENCE 610 AA; 68285 MW; E61310A72FBE739 CRC64;
Query Match 95.7%; Score 3195; DB 2; Length 61c;
Best Local Similarity 99.8%; Pred. No. 1.3e-23; Indels 0; Gaps 0;
Matches 600; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVTQTRPPSWIIICYLWLGFAHTGNAQAKEVLLLDLSKAQOETELEMISPPSGWEISG 60
DB 1 MVTQTRPPSWIIICYLWLGFAHTGNAQAKEVLLLDLSKAQOETELEMISPPSGWEISG 60
QY 61 LDENVYPIRYQVCQWEPNOMNMLRNWISKGAQRIPELKTFLDCKSLPQVLTGCK 120
DB 61 LDENVYPIRYQVCQWEPNOMNMLRNWISKGAQRIPELKTFLDCKSLPQVLTGCK 120
QY 121 EFTNLYYYETDYPDGRNIRENLVYKIDITIADESFTQGDGERMKKNTVREIIGPLSKK 180
DB 121 EFTNLYYYETDYPDGRNIRENLVYKIDITIADESFTQGDGERMKKNTVREIIGPLSKK 180
QY 181 GFYLAFQDVACIALVSVKYYKKCWITVENLAVFPDVTGSEPSLSVEVGTCSAAE 240
DB 181 GFYLAFQDVACIALVSVKYYKKCWITVENLAVFPDVTGSEPSLSVEVGTCSAAE 240
QY 241 EAENSPPMHCSABEEMVPIGCKTCKAGYQOQKGTCPGCGRRYKSSQQLQCSRCTHS 300
DB 241 EAENSPPMHCSABEEMVPIGCKTCKAGYQOQKGTCPGCGRRYKSSQQLQCSRCTHS 300
QY 301 FSDREGSRCECEGGYRAPSDPYVACTPPSPAPOLININQTTVLSLWSPADNGR 360
DB 301 FSDREGSRCECEGGYRAPSDPYVACTPPSPAPOLININQTTVLSLWSPADNGR 360

DB 301 FSDREGSRCECEGGYRAPSDPYVACTPPSPAPOLININQTTVLSLWSPADNGR 360
QY 361 NDVTYRILCKRCSEWQECVPCSGNIGYMPQOTGEDNVTYVMDLAAHYTFEEVANG 420
DB 361 NDVTYRILCKRCSEWQECVPCSGNIGYMPQOTGEDNVTYVMDLAAHYTFEEVANG 420
QY 421 VSDLSRQRLFAVSTTGOAAPSQVSGYMKERVLORSVLSQWQEEHNGVTTEIKY 480
DB 421 VSDLSRQRLFAVSTTGOAAPSQVSGYMKERVLORSVLSQWQEEHNGVTTEIKY 480
QY 481 YEEDQRERTYSLTKTSTASINNLKGTYYVFOIRAVTAAGYNSPRLDVATLBEASG 540
DB 481 YEEDQRERTYSLTKTSTASINNLKGTYYVFOIRAVTAAGYNSPRLDVATLBEASG 540
QY 541 KMEATVASEQNPVITIAVAVAGTIIIVFWVFGTIGRRHCGYSKADQEGDEELYPHS 600
DB 541 KMEATVASEQNPVITIAVAVAGTIIIVFWVFGTIGRRHCGYSKADQEGDEELYPHS 600
QY 601 L 601
DB 601 L 601
RESULT 2
EPAT_MOUSE STANDARD; PRT; 998 AA.
ID EPAT_MOUSE
AC Q61772; Q61505; Q61773; Q61774;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor EHK-3) (EPH homolog kinase-3) (Embryonic brain
DE kinase) (EBK) (Developmental kinase 1) (MDK-1).
GN Name=Epha7; Synonyms=Bk3, Ehk3, Mdk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=95124729; PubMed=7824284;
RA Closek T., Milauer B., Ullrich A.;
RT "Identification of alternatively spliced mRNAs encoding variants of
RT MDK1, a novel receptor tyrosine kinase expressed in the murine nervous
RT system.";
RL Oncogene 10:97-106(1995).
RN [2]
RP SEQUENCE OF 431-998 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=96081374; PubMed=8541219; DOI=10.1016/0925-4773(95)00411-S;
RA Ellis J., Liu Q., Bretzman M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling H.,
RA Fletcher F.A., Ziegler S.F., Rogers J.H.;
RT "Embryo brain kinase: a novel gene of the eph/elk receptor tyrosine
RT kinase family.";
RL Mech. Dev. 52:319-341(1995).
RN [3]
RP INTERACTIONS WITH PRKCA/B AND GRIP1.
RX MEDLINE=9098206; PubMed=9883737; DOI=10.1016/S0896-6273(00)80663-7;
RA Torres R., Firestein B.L., Dong H., Staudinger J., Olson E.N.,
RA Huganir R.L., Bredt D.S., Gale N.W., Yancopoulos G.D.;
RT "PDZ proteins bind, cluster, and synaptically colocalize with Eph
RT receptors and their ephrin ligands.";
RL Neuron 21:1453-1463(1998).
CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC ephrin-A1, -A2, -A3, -A4 and -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Interacts with PRKCA/B and GRIP1.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;

CC	Name=1; Synonyms=MDK1;
CC	Isoid=Q61772-1; Sequence=Displayed;
CC	Name=2; Synonyms=MDK1-1;
CC	Isoid=Q61772-2; Sequence=VSP_003006;
CC	Name=3; Synonyms=MDK1-2;
CC	Isoid=Q61772-3; Sequence=VSP_003007;
CC	Name=4; Synonyms=MDK1-T1;
CC	Isoid=Q61772-4; Sequence=VSP_003008, VSP_003009;
CC	Name=5; Synonyms=MDK1-T2;
CC	Isoid=Q61772-5; Sequence=VSP_003010, VSP_003011;
CC	-1- TISSUE SPECIFICITY: Widely expressed in embryo, in adult,
CC	expression restricted to hippocampus, testis and spleen.
CC	-1- SIMILARITY: Belongs to the Tyr protein kinase family, Ephrin
CC	receptor subfamily.
CC	-1- SIMILARITY: Contains 2 fibronectin type III domains.
CC	-1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC	or send an email to license@isb-sdb.ch).
CC	-----
DR	EMBL; X79082; CAA55687.1; -;
DR	EMBL; X79083; CAA55688.1; -;
DR	EMBL; X79084; CAA55689.1; -;
DR	EMBL; X81466; CAA57224.1; -;
DR	PIR; I48612; I48612.
DR	PIR; I48614; I48614.
DR	PIR; JCS672; JCS672.
DR	HSSP; P54763; IUBA.
DR	MSSP; MG1:95276; EphA7.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR001090; Ephrin_receptor.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR008957; FN_III-like.
DR	InterPro; IPR003962; FNIII_subd.
DR	InterPro; IPR008979; Gal_bind_like.
DR	InterPro; IPR009030; Grow_fac_recept.
DR	InterPro; IPR011009; Kinase_like.
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR001660; SAM.
DR	InterPro; IPR01245; Tyr_kinase.
DR	InterPro; IPR008266; Tyr_kinase_AS.
DR	InterPro; IPR001426; Ykase_receptorV.
DR	Pfam; PF01404; Ephrin_1bd; 1.
DR	Pfam; PF00041; fn3_2.
DR	Pfam; PF00069; Pkinase; 1.
DR	Pfam; PF00536; SAM; 1.
DR	PRINTS; PR00014; FNTYPEPIT.
DR	PRINTS; PR00109; TYRKINASE.
DR	ProDom; PD001495; Ephrin_receptor; 1.
DR	ProDom; PD000001; Prot_kinase; 1.
DR	SMART; SM00615; EPH_1bd; 1.
DR	SMART; SM00060; FN3_2.
DR	SMART; SM00454; SAM; 1.
DR	SMART; SM00219; TyKc; 1.
DR	PROSITE; PS0186; EGF_2; UNKNOWN_1.
DR	PROSITE; PS50853; FN3_2.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR	PROSITE; PS50791; RECEPTOR_TYR_KIN_V_2; 1.
DR	PROSITE; PS50105; SAM_DOMAIN; 1.
KW	Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
KW	Receptor; Repeat; Signal; Transferrase; Transmembrane;
KW	Tyrosine-protein kinase.
FT	SIGNAL 1 29 Potential.
FT	CHAIN 30 998 Ephrin type-A receptor 7.
FT	DOMAIN 30 556 Extracellular (Potential).

[illegible]

Db 421 VSDLSRQRLFAVSTTGOAPSOVSGMKERYLQSRVOLSMQEPHNGVITEYIKY 480
 QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVAATLEBASG 540
 Db 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVAATLEBASG 540
 QY 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGFIIGRHCGYSKADQEDBELEYFH 599
 Db 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGFIIGRHCGYSKADQEDBELEYFH 599
 RESULT 3
 Q8R381 PRELIMINARY; PRT; 994 AA.
 ID Q8R381
 AC Q8R381;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Epha7 protein.
 GN Name=Epha7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2CECH II; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603859;
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udén T.B., Tosliyiuki S., Abramson R.D., Muljany S.J.,
 Raba S.S., Logucliano N.A., Peters G.J., Abramson R.D., Muljany S.J.,
 Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunnaracine P.H.,
 Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.U., Gibbs R.A.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzyzanski M.I., Skalska U., Smallin D.E., Schnerch A., Schain J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C2CECH II; TISSUE=Mammary tumor;
 RC Strausberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 CC -|- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 CC -|- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 CC receptor subfamily.
 CC EMBL: BC026153; AAH26153.1; -.
 DR HSP: P54763; ITPA.
 DR MKD; MG195276; Epha7.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin receptor.
 DR InterPro: IPR003962; PhII subd.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN III-like.
 DR InterPro: IPR008979; Gal bind like.
 DR InterPro: IPR009030; Grow fac recept.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001660; SAM.

DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
 DR InterPro: IPR001426; YKase_receptor_v.
 DR Pfam: PF01404; Ephrin_1bd; 1.
 DR Pfam: PF00041; fn3_1.
 DR Pfam: PF00536; SAM_1.1.
 DR PRINTS; PR00014; ENTPEITII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom: PD001495; Ephrin_receptor; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_1bd; 1.
 DR SMART; SM00060; FN3_2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50853; FN3_2.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS50109; PROTEIN KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 DR ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
 KM Transferase; Transmembrane; Tyrosine-protein kinase
 SQ SEQUENCE 994 AA; 11138 MW; A28F98BD964F2EB8 CRC64;

Query Match 95.5%; Score 3187.5; DB 2; Length 994;
 Best Local Similarity 95.7%; Pred. No. 9.6e-230;
 Matches 604; Conservative 7; Mismatches 15; Indels 5; Gaps 2;

QY 1 MVTQTPSPWIIICITWILGFAHTGEAOAKVLLDLSQAQOTELWISSPPSGMEISG 60
 Db 1 MVTQTPSPWIIICITWILGFAHTGEAOAKVLLDLSQAQOTELWISSPPSGMEISG 60
 QY 61 LDENYPIPTIYQVQWMEPNQNNMLRTNWSKGNARIVELKFTLRDCNSLPVGVGTCK 120
 Db 61 LDENYPIPTIYQVQWMEPNQNNMLRTNWSKGNARIVELKFTLRDCNSLPVGVGTCK 120
 QY 121 ETEFLYYETEDYDGTGNIRENLVYKIDTIADESFTQDGLGERKMLNTEVREIGPLSKK 180
 Db 121 ETEFLYYETEDYDGTGNIRENLVYKIDTIADESFTQDGLGERKMLNTEVREIGPLSKK 180
 QY 181 GFPLAODVAGACALVSVYVYKCKWTIYENLAVFPDVTYSGSFSLVEVRCVSSABE 240
 Db 181 GFPLAODVAGACALVSVYVYKCKWTIYENLAVFPDVTYSGSFSLVEVRCVSSABE 240
 QY 241 EAENSFRMCSABGEMLVPIGKICAKAGYQOKGDTCEPCGRPRYKSSSODLQCSRCPHIS 300
 Db 241 EAENSFRMCSABGEMLVPIGKICAKAGYQOKGDTCEPCGRPRYKSSSODLQCSRCPHIS 300
 QY 301 FSDREGSSRCCEDEGYRPAAPDPYVACTRPPAPQNLIFINQTVLSJEMSPADNGCR 360
 Db 301 FSDREGSSRCCEDEGYRPAAPDPYVACTRPPAPQNLIFINQTVLSJEMSPADNGCR 360
 QY 361 NDVTYIILCKRGWEGEGEYPCGSNIGYMPQDTGLENDYVYVMDLAAHNYFEVAVNG 420
 Db 361 NDVTYIILCKRGWEGEGEYPCGSNIGYMPQDTGLENDYVYVMDLAAHNYFEVAVNG 420
 QY 421 VSDLSRQRLFAVSTTGOAPSOVSGMKERYLQSRVOLSMQEPHNGVITEYIKY 480
 Db 421 VSDLSRQRLFAVSTTGOAPSOVSGMKERYLQSRVOLSMQEPHNGVITEYIKY 480
 QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVAATLEBASG 540
 Db 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVAATLEBASG 540
 QY 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGFIIGRHCGYSKADQEDBELEYFH 600
 Db 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGFIIGRHCGYSKADQEDBELEYFH 600
 QY 601 ---LYRERGDMKTKQHN-KKMMIASGRLL 626
 Db 601 TKTYIDPETYEEDPNAVHQPAKELDASCITKI 631

RESULT 4
 Q8BS08 PRELIMINARY; PRT; 998 AA.
 ID Q8BS08;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length
 DE Enucleated library, clone:5330417H08 product:Eph receptor A7, full
 DE insert sequence.
 GN Name=EphA7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Mech. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y., Itoh M.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Azawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
 RA Adachi J., Azawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hasegaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 CC receptor subfamily.
 DR EMBL; AK030460; BAC26962.1; -.
 DR HSSP; P54763; 1JPA.
 DR MGD; MGI:95276; EphA7.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003962; FnlII_subd.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR011009; Kinase-like.
 DR InterPro; IPR007019; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF01404; Ephrin_1bd; 1.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00536; SAM_1; 1.
 DR PRINTS; PR00014; FNTYPEIIT.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; Eph_1bd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 DR KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
 KW Transferrase; Transmembrane; Tyrosine-protein kinase.
 SQ SEQUENCE 998 AA; 11859 MW; FCA1B83490E746E1 CRC64;
 Query Match 95.5%; Score 3187; DB 2; Length 998;
 Best Local Similarity 99.8%; Pred. No. 1.1e-229;
 Matches 598; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MVVOTRPPSWIILCYIWLGFATGEGQAKEVLLDLSKQOQTELEWISSPPSGMEIRISG 60
 Db 1 MVVOTRPPSWIILCYIWLGFATGEGQAKEVLLDLSKQOQTELEWISSPPSGMEIRISG 60
 Oy 61 LDENVYTRIRYOVQCVMEPNQWMLRTNWSKGNQRIPELKTLLDQNSLPGLGTCK 120
 Db 61 LDENVYTRIRYOVQCVMEPNQWMLRTNWSKGNQRIPELKTLLDQNSLPGLGTCK 120
 Oy 121 ETPFLYYEFDYDGRNIRENLVYKITTIADESFYTGDDGERMKNTVEIREIGPSKK 180
 Db 121 ETPFLYYEFDYDGRNIRENLVYKITTIADESFYTGDDGERMKNTVEIREIGPSKK 180
 Oy 181 GFYLAPODVACIALVSKVYKKCWITVENLAVFPDTVGSSESSLVEVRGTCVSSAEE 240
 Db 181 GFYLAPODVACIALVSKVYKKCWITVENLAVFPDTVGSSESSLVEVRGTCVSSAEE 240
 Oy 241 EAENSPRMHCSAEGEWLVPIGKCI CKAGYQOQKGTCEPCGRRRFYKSSQDLQCSRCPTHS 300
 Db 241 EAENSPRMHCSAEGEWLVPIGKCI CKAGYQOQKGTCEPCGRRRFYKSSQDLQCSRCPTHS 300

QY 301 FSDREGSSRCEDGYRAPSDPPYVACTRPPSAPQMLFININQTVLSLWSPADNGR 360
 DB 301 FSDREGSSRCEDGYRAPSDPPYVACTRPPSAPQMLFININQTVLSLWSPADNGR 360
 QY 361 NDVTYRILCRKCSWEGECPCPGSNIGYMPQGTLEBNYTTWMDLHANYTPEAVNG 420
 DB 361 NDVTYRILCRKCSWEGECPCPGSNIGYMPQGTLEBNYTTWMDLHANYTPEAVNG 420
 QY 421 VSDLSRQRLFAAVSITTGAPSPQSVGMKERVLOASVOLSMOEPHPNGVITEYIKY 480
 DB 421 VSDLSRQRLFAAVSITTGAPSPQSVGMKERVLOASVOLSMOEPHPNGVITEYIKY 480
 QY 481 YEKQQRERTYSTLKTKSTASINNLKRGTYVFPQIRAVTAAGYGNVSPRLVATLEBASG 540
 DB 481 YEKQQRERTYSTLKTKSTASINNLKRGTYVFPQIRAVTAAGYGNVSPRLVATLEBASG 540
 QY 541 KMEPATAVSSSEONPVIIIAVAVAGTIIIVMVGFIIGRRHCGYSKADQIGDELYEH 599
 DB 541 KMEPATAVSSSEONPVIIIAVAVAGTIIIVMVGFIIGRRHCGYSKADQIGDELYEH 599

RESULT 5
 EPAT_RAT STANDARD; PRT; 998 AA.
 ID EPAT_RAT STANDARD; PRT; 998 AA.
 AC P54759;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (Tyrosine-protein
 kinase receptor Etk-3) (EPH homology kinase-3).
 GN Name=Epha7; Synonyms=Etk-3, Etk3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RX MEDLINE=95249272; PubMed=7731712;
 RA Valenzuela D.M., Rojas E., Griffiths J.A., Compton D.L., Gisser M.,
 RA Ip N.Y., Goldfarb M., Yancopoulos G.D.;
 RT "Identification of full-length and truncated forms of Etk-3, a novel
 RT member of the Ebn receptor tyrosine kinase family.";
 RL Oncogene 10:1573-1580(1995).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with PRKCABP and GRIP1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=long;
 CC IsoId=P54759-1; Sequence=Displayed;
 CC Note=More widely expressed in the embryo;
 CC Name=short;
 CC IsoId=P54759-2; Sequence=VSP_003012;
 CC Note=Lacks the kinase domain;
 CC -1- TISSUE SPECIFICITY: Restricted to the nervous system.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; U21954; AAA86830.1; -.

DR EMBL; U21955; AAA86831.1; -.
 DR HSSP; P54763; Jupa.
 DR RGD; 70957; Epha7.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR011009; Kinase-like.
 DR InterPro; IPR007719; Prot_kinase.
 DR InterPro; IPR001650; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; YKase_receptor_V.
 DR Pfam; PR01404; Ephrin_Ibd; 1.
 DR Pfam; PF00041; fn3_2.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; ENTPEIIT.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_Ibd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00853; FN3_2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 DR KAM Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
 DR KMW Receptor; Repeat; Signal; Transferase; Transmembrane;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 24
 FT CHAIN 25 998
 FT DOMAIN 25 556
 FT TRANSMEM 557 577
 FT DOMAIN 578 998
 FT DOMAIN 192 328
 FT DOMAIN 331 433
 FT DOMAIN 443 535
 FT DOMAIN 633 894
 FT DOMAIN 923 987
 FT SITE 998 998
 FT NP_BIND 636 647
 FT BINDING 665 665
 FT ACT_SITE 758 758
 FT MOD_RES 608 608
 FT MOD_RES 614 614
 FT MOD_RES 791 791
 FT MOD_RES 940 940
 FT CARBOHYD 343 343
 FT CARBOHYD 410 410
 FT VARSPIC 600 610

Query 1 MVTQTRPPSWIILCYIWLGFPHATGEAQAKEYLLDSKAQQTLEWISSPPSGMELISG 60
 Best Local Similarity 95.1%; Score 3175; DB 1; Length 998;
 Matches 594; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db      1  MVQTRPSWIIILCYIMLGFAHTGEAQAAKEVLLDLSKAQOTLEWISSPSCGEEISG 60
Qy      61  LDENVYTRIRTYQVQVQWNEPNNMLRTWISKNAQRIFVYLKLTLDQNSLPGVLTGCK 120
Db      61  LDENVYTRIRTYQVQVQWNEPNNMLRTWISKNAQRIFVYLKLTLDQNSLPGVLTGCK 120
Qy      121  ETPFLYYVETDYPDGRNIRENLVYKIDPTIADSFSTQDGLGERKMKLNTREIREIGPLSK 180
Db      121  ETPFLYYVETDYPDGRNIRENLVYKIDPTIADSFSTQDGLGERKMKLNTREIREIGPLSK 180
Qy      181  GFYLAPODVGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSSLVEVAGTCVSSAE 240
Db      181  GFYLAPODVGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSSLVEVAGTCVSSAE 240
Qy      241  EAENSPPMHGABEGEMVLVPIKCI CKAGYQOKGDTCEGGRFYSQSDIQSCRCPHS 300
Db      241  EAENSPPMHGABEGEMVLVPIKCI CKAGYQOKGDTCEGGRFYSQSDIQSCRCPHS 300
Qy      301  FSDREGSSRCCEGQYRAPSDPPVACTRPPSA PNLIFNINOTVYSLEMSPADNGCR 360
Db      301  FSDREGSSRCCEGQYRAPSDPPVACTRPPSA PNLIFNINOTVYSLEMSPADNGCR 360
Qy      361  NDVTYRILCKRCSECEGCVCGSNIGMPOQTGLEDNVYVMDLAAHANYTFEVAVNG 420
Db      361  NDVTYRILCKRCSECEGCVCGSNIGMPOQTGLEDNVYVMDLAAHANYTFEVAVNG 420
Qy      421  VSDLSRSGRFLPANSITTGQAAPSOVSGWKEKRVLONSVOLSMOPBHPNCTVEYEIKY 480
Db      421  VSDLSRSGRFLPANSITTGQAAPSOVSGWKEKRVLONSVOLSMOPBHPNCTVEYEIKY 480
Qy      481  YEKQRERTYSTLTGKTSASINNLKPGTVVFOIRATATAGYGNYSRDLVALTEASG 540
Db      481  YEKQRERTYSTLTGKTSASINNLKPGTVVFOIRATATAGYGNYSRDLVALTEASG 540
Qy      541  KMFEATVSSSQNVIIIAVAVAGTIIIVMVFEGFIIGRHCGYSKADQDELYPH 599
Db      541  KMFEATVSSSQNVIIIAVAVAGTIIIVMVFEGFIIGRHCGYSKADQDELYPH 599

RESULT 6
EPA7_HUMAN STANDARD; PRT; 998 AA.
ID EPA7_HUMAN STANDARD; PRT; 998 AA.
AC Q15375; O9H124;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 7 precursor (BC 2.7.1.112) (Tyrosine-protein
DE kinase receptor EHK-3) (Eph homology kinase-3) (Receptor protein-
DE tyrosine kinase HEK11).
GN Name=EPHA7; Synonym=EHK3, HEK11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Fetal brain;
RX MEDLINE=95206782; PubMed=7898931;
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA Basu R., Welcher A.A.;
RT "cDNA cloning and tissue distribution of five human Eph-like receptor
RT protein-tyrosine kinases.";
RL Oncogene 10:897-905(1995).
RN [2]
RP SEQUENCE OF 1-277 FROM N.A.
RA Bates K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC -1- ephrin-A1, -A2, -A3, -A4 and -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC -1- tyrosine phosphate.
CC -1- SUBUNIT: Interacts with PRKCAP and GRIP1 (By similarity).

```

```

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC receptor subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; L36642; AAA74243.1; -.
DR EMBL; AL121966; CAC19520.1; -.
DR PIR; I58351; I58351.
DR HSSP; P54763; IUPA.
DR Genew; HGNC:3390; EPHA7.
DR MIM; 602190; -.
DR GO; GO:0004714; P:transmembrane receptor protein tyrosine kin. .; TAS.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001090; Ephrin_receptor.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR008979; Gal_bind-like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001660; SAM_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR001426; YKase_receptorV.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; FNIIIPIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; Eph_lbd; 1.
DR SMART; SM00060; FN3_2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS50105; SAM_DOMAIN; 1.
DR ATP-binding; Glycophorin; Receptor; Repeat; Signal;
KW Transferrase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 24
FT CHAIN 1 998
FT DOMAIN 25 556
FT TRANSMEM 557 577
FT DOMAIN 578 998
FT DOMAIN 192 328
FT DOMAIN 331 433
FT DOMAIN 443 535
FT DOMAIN 633 894
FT DOMAIN 923 987
FT SITE 996 998
FT NP_BIND 639 647
FT BINDING 665 665
FT ACT_SITE 758 758
FT MOD_RES 608 608

```

FT	MOD_RES	614	614	Phosphotyrosine (by autocatalysis) (potential).
FT	MOD_RES	791	791	Phosphotyrosine (by autocatalysis) (potential).
FT	MOD_RES	940	940	Phosphotyrosine (by autocatalysis) (potential).
FT	CARBOHYD	343	343	N-linked (GlcNAc. . .) (potential).
FT	CARBOHYD	410	410	N-linked (GlcNAc. . .) (potential).
SEQUENCE	998 AA;	112096 MW;	47983040D2B806EB	CRC64;
Query Match	Best Local Similarity	94.0%;	Score 3139;	DB 1; Length 998;
Matches	585; Conservative	10;	Mismatches	4; Indels 0; Gaps 0;
QY	1	MVQVTRPSWIIICYLWILGFAGHTGEAOAAKEVLLLDLSAQOQTELEWISSPSGMEETISG	60	
DB	1	MVQVTRPSWIIICYLWILGFAGHTGEAOAAKEVLLLDLSAQOQTELEWISSPSGMEETISG	60	
QY	61	LDENTPTIRTVQVQCVMEPNQNNMLRTWISKGNQRI FVELKFTLRQNC LIPGLGICK	120	
DB	61	LDENTPTIRTVQVQCVMEPNQNNMLRTWISKGNQRI FVELKFTLRQNC LIPGLGICK	120	
QY	121	ETPNLYYETDPTDRNIRENLYVYIDTIADESFTQGLGRKKMLTEYREIGPLSK	180	
DB	121	ETPNLYYETDPTDRNIRENLYVYIDTIADESFTQGLGRKKMLTEYREIGPLSK	180	
QY	181	GFYLAFOQVACIALVSVKVVYKKCWITIVENIAVPDVTVGSFSSSLVEVHIGTCVSSAE	240	
DB	181	GFYLAFOQVACIALVSVKVVYKKCWITIVENIAVPDVTVGSFSSSLVEVHIGTCVSSAE	240	
QY	241	EAENSPRHCSAEGEWLVPICKICICKAGYQOKGDPICEPCGRFRFYSSSDI QCSRCPHS	300	
DB	241	EAENAPRHCSAEGEWLVPICKICICKAGYQOKGDPICEPCGRFRFYSSSDI QCSRCPHS	300	
QY	301	FSDRSGSRCECEDERYRAPSDPPYVACTRPPSAQONLIFINQTTVSLHSPADNGCR	360	
DB	301	FSDKSGSRCECEDERYRAPSDPPYVACTRPPSAQONLIFINQTTVSLHSPADNGCR	360	
QY	361	NDVTYRILCKRCSMWQGCVP CGSNGIYMPQQTGLEDNVYVMDLLAAHNTFEVEAVNG	420	
DB	361	NDVTYRILCKRCSMWQGCVP CGSNGIYMPQQTGLEDNVYVMDLLAAHNTFEVEAVNG	420	
QY	421	VSDLSRQRLPFAVSIITGQAAPSOVSGVMKERVQRSYQLSWMQEPHPNVIITYEIKY	480	
DB	421	VSDLSRQRLPFAVSIITGQAAPSOVSGVMKERVQRSYQLSWMQEPHPNVIITYEIKY	480	
QY	481	YEKQDEREYSLTKRSTSSASINNLKPGTVVYFOIRATVAAAGYNSPRLVATLEBASG	540	
DB	481	YEKQDEREYSLTKRSTSSASINNLKPGTVVYFOIRATVAAAGYNSPRLVATLEBASG	540	
QY	541	KMFETAIVASSSEQNPVITIIA VAVAGTIIIVFVWFGIIGRRHCGYSKADQ3GDEELYPH	599	
DB	541	KMFETAIVASSSEQNPVITIIA VAVAGTIIIVFVWFGIIGRRHCGYSKADQ3GDEELYPH	599	
RESULT 7				
ID	Q8C7N2	PRELIMINARY;	PRT;	593 AA.
AC	Q8C7N2;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:CG30003G06 product:Eph receptor A7, full insert			
DE	sequence.			
CN	Name=Epha7;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Hippocampus;			

RX MEDLINE=92979253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed capillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kankawa T.,
 RA Katoh H., Kawai Y., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kuribara K., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK049848; BAC33955.1; --
 DR HSSP; P54763; INUK.
 DR MED; MGI:95276; EphA7.
 DR GO; GO:0005615; Extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001090; Ephrin receptor.
 DR InterPro; IPR003963; FcR1 subd.
 DR InterPro; IPR003964; FN_III like.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR008979; Gal blind like.
 DR InterPro; IPR001426; YKase receptorV.
 DR Pfam; PF01404; Ephrin_Ibd_1.
 DR Pfam; PF00041; fn3_1.
 DR PRINTS; PR00014; EPHYEPHII.
 DR PRODOM; PD001495; Ephrin_receptor; 1.

DR SMART; SM00615; Eph_1bd; 1.
 DR SMART; SM00600; FN3; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR RECEPTOR.
 KW SEQUENCE 593 AA; 66324 MW; 11980225D73F3D83 CRC64;

Query Match 93.6%; Score 3126; DB 2; Length 593;
 Best Local Similarity 99.7%; Pred. No. 1.9e-225;
 Matches 587; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTQTRPSPWIIILCYIMLGFHNGEQAQAEVLLDSKAQOTLEWISSPPSGMEISG 60
 DB 1 MVTQTRPSPWIIILCYIMLGFHNGEQAQAEVLLDSKAQOTLEWISSPPSGMEISG 60
 QY 61 LDENVTPIRTYQVCQVMEPNQNNMLRTNWSKGNQRIFEILKFTLRDQNSLPVGLGTCK 120
 DB 61 LDENVTPIRTYQVCQVMEPNQNNMLRTNWSKGNQRIFEILKFTLRDQNSLPVGLGTCK 120
 QY 121 ETEFLYYETDYGGRNIRENLVYKIDTIADESFTQDGLERKMKLNTREIIGPLSKK 180
 DB 121 ETEFLYYETDYGGRNIRENLVYKIDTIADESFTQDGLERKMKLNTREIIGPLSKK 180
 QY 181 GFYLAPODVGACIALVSVKYVYKKCWITVENLAVFPDVTGSEFSLVEVAGTCVSSAE 240
 DB 181 GFYLAPODVGACIALVSVKYVYKKCWITVENLAVFPDVTGSEFSLVEVAGTCVSSAE 240
 QY 241 EAENSPRMHCAGEBMLVPICKICIKAGYQOKGDTCEPCGRFPYKSSQDIQCSRCPTHS 300
 DB 241 EAENSPRMHCAGEBMLVPICKICIKAGYQOKGDTCEPCGRFPYKSSQDIQCSRCPTHS 300
 QY 301 FSDREGSRCECEGYVAPSDPPVACTRPPSAQNIIFINQTTVLEWSPADNGR 360
 DB 301 FSDREGSRCECEGYVAPSDPPVACTRPPSAQNIIFINQTTVLEWSPADNGR 360
 QY 361 NDVTYRIICKRCSMEQECVPCGSNIGVPOQTGLEDDYVYVMDLAANTFEVAVNG 420
 DB 361 NDVTYRIICKRCSMEQECVPCGSNIGVPOQTGLEDDYVYVMDLAANTFEVAVNG 420
 QY 421 VSDLSRSGRLFAAASITTTGAAPSGVSMKERVLRQSVQSWQEPHPNGVITEYEIKY 480
 DB 421 VSDLSRSGRLFAAASITTTGAAPSGVSMKERVLRQSVQSWQEPHPNGVITEYEIKY 480
 QY 481 YEKQRETTYSTLTKTSASINMLKEGTYYVFOIRANTAGYGYNSRLDVATLEASG 540
 DB 481 YEKQRETTYSTLTKTSASINMLKEGTYYVFOIRANTAGYGYNSRLDVATLEASG 540
 QY 541 KMFEATAVSSSEONPVIIIAVAVAGTILVFMVFGFIIGRRHCGYSKAD 589
 DB 541 KMFEATAVSSSEONPVIIIAVAVAGTILVFMVFGFIIGRRHCGYSKAE 589

RESULT 8
 EPI7 CHICK STANDARD; PRT; 993 AA.
 AC 042422;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-2 receptor 7 precursor (BC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor CBPAH7) (Tyrosine-protein kinase receptor CEK11).
 GN Name=EphA7; Synonyms=CEK11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=98092111; PubMed=9431814; DOI=10.1016/S0925-4773(97)00147-0;

RA Araujo M., Nieto M.A.;
 RT "the expression of chick EphA7 during segmentation of the central and
 RT peripheral nervous system.";
 .RL Mech. Dev. 68:173-177(1997).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Within the nervous system, expression is
 CC restricted to prosomeres 1 and 2 in the diencephalon and all the
 CC rhombomeres in the hindbrain during segmentation stages. Later on,
 CC a superimposed pattern appears that correlates with the formation
 CC of several axonal tracts. In the somitic mesoderm, the expression
 CC correlates with segmentation and the guidance of both neural crest
 CC and motor axons through the sclerotomes.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; Y14271; CA474643.1; -.
 DR HSSP; P54763; IUPA.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-1like.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR008979; Gal_Bind_1like.
 DR InterPro; IPR009030; Gw_Fac_recept.
 DR InterPro; IPR011009; Kinase_1like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; Ykase_receptolv.
 DR Pfam; PF01404; Ephrin_1bd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; kinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIIT.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; Eph_1bd; 1.
 DR SMART; SM00600; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
 KW Transferrase; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 30
 FT CHAIN 31 993
 FT DOMAIN 31 551
 FT TRANSMEM 552 572
 FT DOMAIN 573 993
 FT DOMAIN 192 328
 FT DOMAIN 331 433
 FT DOMAIN 443 535

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FT DOMAIN 628 889 Protein kinase.
FT 918 982 SAM.
FT SITE 991 993 PDZ-binding motif (potential).
FT NP_BIND 634 642 ATP (By similarity).
FT DISULFID 74 109 ATP (By similarity).
FT BINDING 660 660 ATP (By similarity).
FT ACT_SITE 753 753 By similarity.
FT MOD_RES 603 603 Phosphotyrosine (by autocatalysis)
FT MOD_RES 609 609 Phosphotyrosine (by autocatalysis)
FT MOD_RES 786 786 Phosphotyrosine (by autocatalysis)
FT MOD_RES 935 935 Phosphotyrosine (by autocatalysis)
FT MOD_RES 935 935 Phosphotyrosine (by autocatalysis)
FT CARBOHYD 343 343 N-linked (GlcNAc...) (potential).
FT CARBOHYD 410 410 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 993 AA; 111366 MW; EECF9603047608BD CRC64;

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Query Match 90.8%; Score 3031.5; DB 1; Length 593;
Best Local Similarity 94.5%; Pred. No. 4,7e-218;
Matches 566; Conservative 17; Mismatches 11; Indels 5; Gaps 1;

QY 1 MVVQTRPSMIIICVIMLGFAGHGAQAQKVVLLDSKAQQTLEWISGPPSGMEISG 60
D 1 MVLRSRLPMMICSVMLRPAHGAQAQKVVLLDSKAQQTLEWISGPPSGMEISG 60
QY 1 LDENYPIRTYQVQVMEPNQNMRLRTNMISKGNAGRIFFELKFTLLDCKSLPGVLGTCK 120
D 1 LDENYPIRTYQVQVQVMEPNQNMRLRTNMISKGNAGRIFFELKFTLLDCKSLPGVLGTCK 120
QY 121 ETEFNLYYEFDYDGTGRNIRENLYKIDTIADESFTGDI GERMKINTVREIGPSKK 180
D 121 ETEFNLYYEFDYDGTGRNIRENLYKIDTIADESFTGDI GERMKINTVREIGPSKK 180
QY 121 ETEFNLYYEFDYDGTGRNIRENLYKIDTIADESFTGDI GERMKINTVREIGPSKK 180
D 121 ETEFNLYYEFDYDGTGRNIRENLYKIDTIADESFTGDI GERMKINTVREIGPSKK 180
QY 181 GFYIAFDVACIALYVVKYKKCWITVNIANFPTVVGSESSIVRGCVSAAE 240
D 181 GFYIAFDVACIALYVVKYKKCWITVNIANFPTVVGSESSIVRGCVSAAE 240
QY 181 GFYIAFDVACIALYVVKYKKCWITVNIANFPTVVGSESSIVRGCVSAAE 240
D 181 GFYIAFDVACIALYVVKYKKCWITVNIANFPTVVGSESSIVRGCVSAAE 240
QY 241 EAENSPPMHCSAEGEWLVPIGKICIKAGYQOKGDTCPGCRPFYKSSSOTLQSCRPTHS 300
D 241 EAENSPPMHCSAEGEWLVPIGKICIKAGYQOKGDTCPGCRPFYKSSSOTLQSCRPTHS 300
QY 241 EAENSPPMHCSAEGEWLVPIGKICIKAGYQOKGDTCPGCRPFYKSSSOTLQSCRPTHS 300
D 241 EAENSPPMHCSAEGEWLVPIGKICIKAGYQOKGDTCPGCRPFYKSSSOTLQSCRPTHS 300
QY 301 FSPDESSRCECEDGYRAPSDPPYACTPPSPAPQNLININQTVSLIWSPPADNGR 360
D 301 FSPDESSRCECEDGYRAPSDPPYACTPPSPAPQNLININQTVSLIWSPPADNGR 360
QY 301 FSPDESSRCECEDGYRAPSDPPYACTPPSPAPQNLININQTVSLIWSPPADNGR 360
D 301 FSPDESSRCECEDGYRAPSDPPYACTPPSPAPQNLININQTVSLIWSPPADNGR 360
QY 361 NDVTYRILCRCSWEGECVPCGSGNIGYMPQGTGLVDNYVTVDLHANAYTEVEAVNG 420
D 361 NDVTYRILCRCSWEGECVPCGSGNIGYMPQGTGLVDNYVTVDLHANAYTEVEAVNG 420
QY 361 NDVTYRILCRCSWEGECVPCGSGNIGYMPQGTGLVDNYVTVDLHANAYTEVEAVNG 420
D 361 NDVTYRILCRCSWEGECVPCGSGNIGYMPQGTGLVDNYVTVDLHANAYTEVEAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGAAPSOVSGWKKERVLQSRVOLSMQEPHNPVITTEYRIKY 480
D 421 VSDLSRSQRLFAAVSITTTGAAPSOVSGWKKERVLQSRVOLSMQEPHNPVITTEYRIKY 480
QY 421 VSDLSRSQRLFAAVSITTTGAAPSOVSGWKKERVLQSRVOLSMQEPHNPVITTEYRIKY 480
D 421 VSDLSRSQRLFAAVSITTTGAAPSOVSGWKKERVLQSRVOLSMQEPHNPVITTEYRIKY 480
QY 481 YEKDQRRRTYSTLKTSKTSASINNLKPGTYVFOIRAATAAGYGNVSPRI DVATLEBASG 540
D 481 YEKDQRRRTYSTLKTSKTSASINNLKPGTYVFOIRAATAAGYGNVSPRI DVATLEBASG 540
QY 481 YEKDQRRRTYSTLKTSKTSASINNLKPGTYVFOIRAATAAGYGNVSPRI DVATLEBASG 540
D 481 YEKDQRRRTYSTLKTSKTSASINNLKPGTYVFOIRAATAAGYGNVSPRI DVATLEBASG 540
QY 541 KMREATAVSSQNVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADLEGDEBELYFH 599
D 541 KMREATAVSSQNVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADLEGDEBELYFH 599
QY 541 KMREATAVSSQNVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADLEGDEBELYFH 599
D 541 KMREATAVSSQNVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADLEGDEBELYFH 599

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DE insect sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/15055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komno H., Akiyama U., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089143; BAC40764.1; -.
DR HSSP; P54763; INDK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005003; F:protein receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:000468; F:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.

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DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin receptor.
 DR InterPro: IPR003962; Fcrl1 subd.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR008979; Gal bind like.
 DR InterPro: IPR009030; Grow_fac recept.
 DR InterPro: IPR001426; Ykase_receptor.
 DR Pfam: PF001404; Ephrin_1bd_1.
 DR Pfam: PF000041; fn3_2.
 DR PRINTS: PR00014; FNTYPEIII.
 DR ProDom: PD001495; Ephrin_receptor_1.
 DR SMART: SM00615; EPH_1bd_1.
 DR SMART: SM00605; FN3_2.
 DR PROSITE: PS00186; EGF_2_1.
 DR PROSITE: PS50853; FN3_2.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1_1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2_1.
 KM Receptor.
 SQ SEQUENCE 681 AA; 75336 MW; 92B9187AB78BE722 CRC64;

Query Match 55.7%; Score 1860.5; DB 2; Length 681;
 Best Local Similarity 57.1%; Pred. No. 1.5e-130;
 Matches 349; Conservative 97; Mismatches 134; Indels 31; Gaps 8;

QY 6 RFPSSWIIICY-----IW-----LLGFHTGBAQAKVLLDLSKAQQTLEWISPPSG 54
 DB 25 RVPSLSLACGYAPLKGPMITCLLCALRTLLASPSNEVNLIDRTWGDLCWIAFPKNG 84
 QY 55 WEIISGLDENTYPIRTYQVCVMEBPNQNNMLRTNWSKGNQRIFEVLKFTLRDQNSLPG 114
 DB 85 WEIIGEDVENYAPLHTYQVCVMEQNNMLLTWSISNEGSRIFELKFTLRDQNSLPG 144
 QY 115 VLGTCKETFNLYYETDYDTGRNIRENLYKIDTIADESTQGLDGRKKKLTVEREI 174
 DB 145 GLGTCKETFNMYETDSDENGRSISENQYKIDTIADESFTELDLGRVKKLTVERADV 204
 QY 175 GPLSKGPFYLAFOVGVACIALVSVKVVYKKCKMTIENLAVPDPYATGSEFSISLVEVRGT 234
 DB 205 GPLSKGPFYLAFOVGVACIALVSVKVVYKKCPVVRHLATFPDITIGDSSQLAEVSGSC 264
 QY 235 VSSAEENENSPRMHCSAEGEMLVPIGKCIKAGYQCKGDTCEPCGRFRFYKSSQDLOCS 294
 DB 265 VN--HSVTDDPRKHKCSAEGEMLVPIGKCMCKAGEEKNGTCQYCRPGFKASPHSQCS 322
 QY 295 RCPHTSSDRGSSRCBCEDGYTPAPSDPYVACTRPPSAQNLIFNINQTVSLIENSP 354
 DB 323 KCPHSTYHERASTSCVCEKDYFRKDSPPPTMACTRPPSAPRNAISNNEFVSFLEWITP 382
 QY 355 ADNGGRDVTYRIICKKCSMEQGEVPCGSNIGWVPOOTGLDNYVTYMDLLAHANTFE 414
 DB 383 ADTGGRDVTYRIICKKCSNAGVCEEGCHVRHLPQDILKNSVMMVDDLAHNTYFE 442
 QY 415 VEAVNGVSDLSRQRLFAAIVITGQAAPSQVSGVMKERVLRQSVOLSMQEPHNGVIT 474
 DB 443 IEAVNGVSDLSRQRLFAAIVITGQAAPSQVSGVMKERVLRQSVOLSMQEPHNGVIT 502
 QY 475 EYEIKTYEKQREKTYSTLTKTSASANNLKPGTVYFQIRAYTAAGYGYSPRLDYAT 534
 DB 503 EYEIKTYEKQD-ETSYTIKSKETSITAEGLKPASVYFQIRARAAAGYGYFSRFE-- 558
 QY 535 LBAASGMKFEAT-----AVSSEONPIITIAVAVAGTIIIVMVGFIIGRHGCGSKADQ 590
 DB 559 -----FETTPVSVASANDSQIPIITAVSVTVGVILLAVMT-GFLLSGRRCGISYKQ 609
 QY 591 EGDEE-LYFHS 600
 DB 610 DPBEKKMHFN 620

RESULT 10
 EPAS_RAT STANDARD; PRT; 1005 AA.

AC P54757;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor EHK-1) (EPH homology kinase-1).
 GN Name=EphA5; Synonyms=Ehk-1, Ekh1;
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=94067777; PubMed=7504232;
 RA Maisompierre P.C., Barrezaeta N.X., Yancopoulos G.D.;
 RT "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine
 RT kinase family with distinctive structures and neuronal expression.";
 RL Oncogene 8:3277-3288(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=95206467; PubMed=7898646; DOI=10.1016/0306-4522(94)90014-0;
 RA Taylor V., Miescher G.C., Pfeiffer S., Honegger P., Breitschopf H.,
 RA Laessmann H., Steck A.U.;
 RT "Expression and developmental regulation of Ehk-1, a neuronal Elk-like
 RT receptor tyrosine kinase in brain";
 RL Neuroscience 63:163-178(1994).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: Type I membrane protein.
 CC Event=Alternative splicing; Named isoforms=6;
 CC Name=1;
 CC IsoId=P54757-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P54757-2; Sequence=VSP_003001;
 CC Name=3;
 CC IsoId=P54757-3; Sequence=VSP_003002;
 CC Name=4;
 CC IsoId=P54757-4; Sequence=VSP_003002, VSP_003003;
 CC Name=5;
 CC IsoId=P54757-5; Sequence=VSP_003001, VSP_003002, VSP_003003;
 CC Name=6;
 CC IsoId=P54757-6; Sequence=VSP_003000, VSP_003002;
 CC -1- TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
 CC system. Predominantly expressed in neurons.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC -----
 CC EMBL: X78689; CAAS5357.1; -.
 CC PIR: S49015; S49015.
 CC PIR: S51603; S51603.
 CC HSSP: P54763; 1JPA.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin receptor.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003962; Fcrl1 subd.
 DR InterPro: IPR008979; Gal_bind like.
 DR InterPro: IPR009030; Grow_fac_recept.

DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_Kinase.
DR InterPro; IPR008266; Tyr_Kinase_AS.
DR InterPro; IPR001426; YKase_receptorV.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PRO0014; FNTYPEIII.
DR PRINTS; PRO0109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00615; Eph_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS01166; EGF_2; UNKNOWN_1.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS5105; SAM_DOMAIN; 1.
KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
KW Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
KM
FT CHAIN 1 26 By similarity.
FT TRANS 27 1005 Ephrin type-A receptor 5.
FT TRANS 27 575 Extracellular (Potential).
FT TRANS 576 596 Potential.
FT DOMAIN 597 1005 Cytoplasmic (Potential).
FT DOMAIN 222 356 Cys-rich.
FT DOMAIN 359 461 Fibronectin type-III 1.
FT DOMAIN 471 561 Fibronectin type-III 2.
FT DOMAIN 677 938 Protein kinase.
FT DOMAIN 967 1005 SAM.
FT NP_BIND 683 691 ATP (By similarity).
FT BINDING 709 709 ATP (By similarity).
FT ACT_SITE 802 802 By similarity.
FT MOD_RES 652 652 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 658 658 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 835 835 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 835 835 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 984 984 Phosphotyrosine (by autocatalysis) (By similarity).
FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 301 301 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 425 425 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 438 438 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
FT VARSPPLIC 10 20 GRRRTGGRGG->DADGPRADSWCHARR (in isoform 6).
FT VARSPPLIC 306 357 /FTid=VSP_003000.
FT VARSPPLIC 306 357 VCRPGFKASPHSGTCKPCPHSYTHBEATSCVCKDYPR
FT RESDPRMFACT->G (in isoform 2 and isoform 5).
FT VARSPPLIC 358 470 /FTid=VSP_003001.
FT VARSPPLIC 358 470 RPPAPRNAISNNVETSVFLEWIPPADTGCCKDVSYVILCK
FT CKNSHAGVCEGCHVYLLQOIGLKTYSVMADPLAHYV
FT TFEIEAVNGVSDLSPGTRGVVSVVVTNQA->T (in isoform 3, isoform 4, isoform 5 and isoform 6).
FT VARSPPLIC 597 621 /FTid=VSP_003002.
FT VARSPPLIC 597 621 SGSCCEGCGRASSLCVAHPSLIW->R (in isoform 4 and isoform 5).
FT CONFLICT 170 170 D->E (in Ref. 2).
FT CONFLICT 566 566 G->A (in Ref. 2).

FT CONFLICT 578 578 G->A (in Ref. 2).
FT CONFLICT 669 669 G->A (in Ref. 2).
FT CONFLICT 708 708 T->I (in Ref. 2).
FT CONFLICT 979 979 T->I (in Ref. 2).
SQ SEQUENCE 1005 AA; 111007 MW; 1AED42C99693C574 CRC64;
Query Match 54.5%; Score 1819; DB 1; Length 1005;
Best Local Similarity 55.1%; Pred. No. 3,4e-127;
Matches 348; Conservative 96; Mismatches 136; Indels 52; Gaps 10;
QY 6 RPSWIIICV-----IW-----LGFPHGGEQAQKEVILLNSKQQTLEWISSPSG 54
DB 25 RVPASLAGCTSAPLKPKLMTCLLLCALRTLLSPSEVNLDSRYVLGDLGIAPKNG 84
QY 55 WEISGLDENVTPIRTYQVCQVMEPNQWMLRTNWSKNAQRIPVELKTLTLDNSLPG 114
DB 85 WEIEGVDENVTAPIHRTYQVCQVMEQNMWMLLSWISNBASNIFIELKTLTLDNSLPG 144
QY 115 VLGTCKETFMVLYYEDYDTGRNIRENLVYKIDITIADESFTGGDLAGRRMKLNTVEYR 174
DB 145 GLGTCKETFMVLYYEDYDTGRNIRENLVYKIDITIADESFTELDGDGRVYKLNTEYRDV 204
QY 175 GPLSKGFTYLAPODVACIALVSVKYYKKCWITVENLAVFPPTVGSSESSLVEYRGTG 234
DB 205 GPLSKGFTYLAPODVACIALVSVKYYKKCPVSHLAVFPPTITGADSSQLLEVSQSC 264
QY 235 VSSAEBAENSPPMHGSAEGEVLVPIGKICIKAGYQOKGDTCEPCGRRFYKSSODLQCS 294
DB 265 VN--HSVTDPRPMHGSABGEMLVPIGKCMCKAGYEENKGTQVCRPGFKAPHSQTC 322
QY 295 RCTHSPSDREGSSRCEDEGYTRAPSDPPYACTRPPAPQVLIRINQTTVLSKSP 354
DB 323 KCPHSTHTEASTSCVCEKDYFRRESDEPTAPCPAPRAVAISNVETSVFLEWIP 382
QY 355 ADNGRNDVYRILTKRCGSEGEVCPGCSNIGYMOQGTLENYTVMDLHAHYTFE 414
DB 383 ADTGCGKDVSYLLCKCKSHAGVCEGCHVYLLQOIGLKTYSVMADPLAHYTFE 442
QY 415 VEAVNGVSDLSRSQRLPAVSIITGQAPSOYGVWKEKRYLQSRVOLSQDEPHNGVIT 474
DB 443 IEAVNGVSDLSPTQRYVSNVTNQAAPSPVNVKKGAKAKNISLSWQDEPRPGIIL 502
QY 475 EYIKTYEKDQRRYVSTLTKSTASINNLKGYVYVQIRAVTYAGGNSPRLDVAT 534
DB 503 EYIKTYEKDQ--ETSYTIKSKETITTAGLKPASVYVQIRARITAGYGVFSRPE--- 558
QY 535 LBEASGMPFATV---SSRQNPVITIAVAVAGTIIIVMGVGFII-----GRR- 581
DB 559 -----FETTVFPGASNDQSIPIITIGSVYGVILLAVMI-GFLLSGSCCEGCGRAS 609
QY 582 -----HCGYSKADQDEGDEE-LYFHS 600
DB 610 SLCAVAHPSLIWICGYSKAKQDPEEKMHFN 641
RESULT 11
ID EPAS_HUMAN STANDARD; PRT; 1037 AA.
AC P54756;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EHK-1) (Bph homology kinase-1) (Receptor protein-tyrosine kinase HEK7).
DE Name=EPH45; Synonyms=EHK1, HEK7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homiindae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

RA Miescher G.C.;
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 25-1037 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95206782; PubMed=7898931;
 RA Fox G.M., Wolcher P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
 BA Baeu R., Helcher A.A.;
 RT "cDNA cloning and kinase distribution of five human Eph-like receptor
 protein-tyrosine kinases";
 RL Oncogene 10:897-905(1995).
 CC -1 FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P54756-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P54756-2; Sequence=VSP_002999;
 CC -1 TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
 CC system.
 CC -1 SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -1 SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X95425; CAN64700.1; -;
 DR EMBL: L36644; AAA74245.1; -;
 DR HSSP: P54763; IUPA.
 DR Genew; HGNC:3389; IUPA5.
 DR MIM; 600004; -;
 DR GO: GO:0016021; C:Integral to membrane; TAS.
 DR GO: GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR001090; Ephrin_receptor.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003962; FNIII_subd.
 DR InterPro: IPR008879; Gal_bind_like.
 DR InterPro: IPR009030; Grow_fac_recept.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001660; SAM.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
 DR InterPro: IPR001426; Ykase_receptorV.
 DR Pfam: PF00404; Ephrin_lbd; 1.
 DR Pfam: PF00041; FN3; 2.
 DR Pfam: PF00069; Kinase; 1.
 DR PRINTS: PR00014; FNTYPEIIT.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRODOM: PD001495; Ephrin_receptor; 1.
 DR PRODOM: PD000001; Prot_kinase; 1.
 DR SMART: SM00615; EPH_lbd; 1.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00454; SAM; 1.
 DR SMART: SM00219; TYRKC; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS50853; FN3; 2.

DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS50105; SAM DOMAIN; 1.
 KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
 KW Receptor; Repeat; Signal; Transferrase; Transmembrane;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 24
 FT CHAIN 25 1037 Potential.
 FT EPHRIN type-A receptor 5.
 FT TRANSMEM Extracellular (Potential).
 FT TRANSMEM Potential.
 FT DOMAIN 574 594 Cytoplasmic (Potential).
 FT DOMAIN 595 1037 Cys-rich.
 FT DOMAIN 220 354 Fibronectin type-III 1.
 FT DOMAIN 357 459 Fibronectin type-III 2.
 FT DOMAIN 469 559 Fibronectin type-III 2.
 FT DOMAIN 675 936 Protein kinase.
 FT DOMAIN 965 1029 SAM.
 FT SITE 1035 1037 PDZ-binding motif (Potential).
 FT NP_BIND 681 689 ATP (By similarity).
 FT BINDING 707 707 ATP (By similarity).
 FT ACT_SITE 800 800 By similarity.
 FT MOD_RES 650 650 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 656 656 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 833 833 Phosphotyrosine (by autocatalysis) (Potential).
 FT MOD_RES 982 982 Phosphotyrosine (by autocatalysis) (By similarity).
 FT CARBOHYD 264 264 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 299 299 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 423 423 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 436 436 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 461 461 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 597 619 SCCEGCGGRASLCAVAHPILIW -> R (in isoform 2).
 FT FT
 SQ SEQUENCE 1037 AA; 114784 MW; FC2C46C959AFB699 CRC64;
 Query Match 54.4%; Score 1817; DB 1; Length 1037;
 Best Local Similarity 55.5%; Pred. No. 5e-127;
 Matches 346; Conservative 97; Mismatches 132; Indels 48; Gaps 10;
 QY 6 RPSW--IICYLWLGFAHGEAQAKEVLLDSKAQTELEWISSPSCWMEISGLDE 63
 DB 37 RAPLMTCLLC-----AALRTLLASPSNEVALLDSRTVMGDLGIAPFKNGMEIEGEVDE 91
 QY 64 NYTPIRTYQVQVQVNEPQNNMLRTNMTSKGAQRIFVEIKRTLLDQNSLPGLGTCKETP 123
 DB 92 NYAPLHYQVCKVQVQNNMLLTWSINBEGASPIFLKRTLLDQNSLPGLGTCKETP 151
 QY 124 NLVYETDYPDGRNIRENLYKIDITIADESFQGDGERKQKNTREIREISPKSKGFY 183
 DB 152 NMYTFESPQDQGRNIRENLYKIDITIADESFQGDGERKQKNTREIREISPKSKGFY 211
 QY 184 LAFQDVGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSIVVRGTCVSSAAEBEAE 243
 DB 212 LAFQDVGACIALVSVRYYKKCPVIRHLAVFPDITIGADSSQLLEVGSCV--HSTVD 269
 QY 244 NSPRMGASGEEMLVPIGKCI CKRGYQOKGTCEPCGRFRFKSSQDLQRCRCPTHSPSD 303
 DB 270 EPPKMGASGEEMLVPIGKCI CKRGYQOKGTCEPCGRFRFKSSQDLQRCRCPTHSPSD 329
 QY 304 REGSSRCCEDEGYRAASDPYVACTRPPAPQNLIFINQTVLSLEWSPADNGGRNDV 363
 DB 330 EEAISTCVCEDYRRRESDEPTMACTRPPAPRAIASVAVETSVFLFEMIPADTGCRKDV 389
 QY 364 TYRILCRGSGEGECVPCGSNIGYMPQQTGLDENVTYVMDLAAHYNTFEVAANGVSD 423
 DB 390 SYTIACKCKNSHAGVCECGGHVRYVLPROSGLKNTSVVMVDLLAHNTYTFEIEAVNGVSD 449

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QY 424 LSRGRLFAAVSITTTGAAPSOVSGWKKERYLQSRVOLSGQEPHNPVITEYEIKYXK 483
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 450 LSPCARQVSVNVTNQAAISPVTNVKGIANKSISLSMQEPRPFGIIILEYEIKHFEK 509
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 484 DQERRTSTLKTSTASINNLKRGTYVQIRAVTAAGGNVSPRLDVATLEBAGKMF 543
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 510 DQ-ETSYTIKSKETTTAGLKPKASVYVQIRARTAGVGFSPRPE-----F 557
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 544 EAT---AVSSEONVLIIVAVAGTIIIVMGVFI-----GRR----- 581
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 558 ETTVPVFASSDQSGIPVIANSVTVG-VILLAVIGVLSGSCCGCGRASSLCAVAHPI 616
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 582 ---HCGYSKADQEGDEE-LYFHS 600
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 617 LWRGCGYKAKQDPEEKMFHN 639
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

RESULT 12
EPAS_CHICK STANDARD; PRT; 1013 AA.
ID EPAS_CHICK
AC P54755; 007495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor CEK7).
GN Name=EPHNA5; Synonyms=CEK7;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body wall;
RX MEDLINE=95047429; PubMed=7958948; DOI=10.1016/0378-1119(94)90692-0;
RA Stever D.A., Verderame M.F.;
RT "Identification of a complete Cdk7 receptor protein tyrosine kinase
RT coding sequence and cDNAs of alternatively spliced transcripts.";
RL Gene 148:219-226(1994).
RN [2]
RP SEQUENCE OF 512-1013 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93288394; PubMed=8510926;
RA Sajjadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed."
RL Oncogene 8:1807-1813(1993).
CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC ephrin-A1, -A2, -A3, -A4 and -A5. Able to collapse growth cones.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=3;
CC IsoId=P54755-1; Sequence=Displayed;
CC Name=1;
CC IsoId=P54755-2; Sequence=VSP_003005;
CC Name=2;
CC IsoId=P54755-3; Sequence=VSP_003004, VSP_003005;
CC -1- TISSUE SPECIFICITY: Detected in the 10-day embryonic brain, weaker
CC expression in the rest of the 10-day embryo. Undetected in adult
CC tissues.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC receptor subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U03910; AAB60613.1; -
CC EMBL; U03910; AAB60614.1; -
CC EMBL; U03910; AAB60612.1; -
CC EMBL; Z19058; CAA79508.1; -.
CC PIR; I50615; I50615.
CC HSSP; P54763; IUPA.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR001090; Ephrin_receptor.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003962; FNIII subd.
CC InterPro; IPR008979; Gal_bind_like.
CC InterPro; IPR009030; Grow_fac_recept.
CC InterPro; IPR011009; Kinase_like.
CC InterPro; IPR00719; Prot_kinase.
CC InterPro; IPR001660; SAM_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC InterPro; IPR008266; Tyr_kinase_AS.
CC InterPro; IPR001426; YKase_receptor_V.
CC Pfam; PF00404; Ephrin_1bd; 1.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00069; Kinase; 1.
CC Pfam; PF00536; SAM; 1.
CC PRINTS; PR00014; ENTYPERII.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD001495; Ephrin_receptor; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00615; EPH_1bd; 1.
CC SMART; SM00060; FN3_2.
CC SMART; SM00454; SAM; 1.
CC SMART; SM00219; TYKc; 1.
CC PROSITE; PS01186; EGF_2; UNKNOWN_1.
CC PROSITE; PS50853; FN3; 2.
CC PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50117; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS50019; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
CC PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
CC PROSITE; PS50105; SAM_DOMAIN; 1.
CC KW Alternate splicing; ATP-binding; Glycoprotein; Phosphorylation;
CC Receptor; Repeat; Signal; Transferrase; Transmembrane;
CC Tyrosine-protein kinase.
CC SIGNAL 1 31 Potential.
CC CHAIN 32 1013 Ephrin type-A receptor 5.
CC DOMAIN 32 549 Extracellular (Potential).
CC TRANSMEM 550 570 Potential.
CC DOMAIN 571 1013 Cytoplasmic (Potential).
CC DOMAIN 196 330 Cys-rich.
CC DOMAIN 333 435 Fibronectin type-III 1.
CC DOMAIN 445 535 Fibronectin type-III 2.
CC DOMAIN 651 912 Protein kinase.
CC DOMAIN 941 1013 SAM.
CC SITE 1011 1013 PDZ-binding motif (Potential).
CC NP_BIND 657 665 ATP (by similarity).
CC BINDING 683 683 ATP (by similarity).
CC ACT_SITE 776 776 By similarity.
CC MOD_RES 626 626 Phosphotyrosine (by autocatalysis) (By
CC similarity).
CC MOD_RES 632 632 Phosphotyrosine (by autocatalysis) (By
CC similarity).
CC MOD_RES 809 809 Phosphotyrosine (by autocatalysis)
CC (Potential).
CC MOD_RES 958 958 Phosphotyrosine (by autocatalysis) (By
CC similarity).
CC CARBOHYD 240 240 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 275 275 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 345 345 N-linked (GlcNAc...) (Potential).

```



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DR GO:0005003; F:ephrin receptor activity; IDA.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR001090; Ephrin_receptor.
DR InterPro: IPR003962; Fcrl1_subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR008979; Gal_Bind_like.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR001660; SAM_2.
DR InterPro: IPR011510; SAM_2.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR InterPro: IPR001426; Ykase_receptor.
DR Pfam: PF00041; Efnrln_lbd.1.
DR Pfam: PF00041; Efnrln_lbd.1.
DR Pfam: PF07647; SAM_2; 1.
DR PRINTS: PR00014; FNTYPEIIT.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD001495; Ephrin_receptor; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00615; EPH_lbd; 1.
DR SMART: SM00060; FN3_2.
DR SMART: SM00454; SAM; 1.
DR SMART: SM00219; TYRKC; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00853; FN3_2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS0105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transmembrane; Tyrosine-protein kinase
SQ SEQUENCE 984 AA; 110037 MW; B4CB810EB34D078 CRC64;

Query Match 53.9%; Score 1799; DB 2; Length 984
Best Local Similarity 56.8%; Pred. No. 1e-125;
Matches 336; Conservative 103; Mismatches 135; Indels :8; Gaps 7;

QY 13 LCYIMLIG--FAHTGE--AQAKEVILLDSKAQOTLEWISSPPSGME--SGLDENYTP 67
DB 5 LSLVLLGCCVLSGSGELSPQSPNEVLLDSKTIQGLGWISYPSHGMEE:SGVDENYTP 64
QY 68 IRTYQVCQWEPNQNMLRTNWSKGAORIPVELKFTLLDCNSLPGLGCKETPNLYY 127
DB 65 IRTYQVCNVDHSDONMLRTNWPFRNSAOKIYVELKFTLLDCNSIPVLGTCETPNLYY 124
QY 128 YETDYDTGRNIRENTLVYKIDTIADESFQDGLGERKMKUNTEVREIGPL3KKGFYLAFO 187
DB 125 MESDDHGVAFREHQFTKIDTIADESFQMDGDRILKUNTEIREVGVYKKGFIYLAFO 184
QY 188 DVGACILAVSVKYYKKCGMTIVENLAVFPPTVTGSESSSLVEVRGTCVSS4EEBAENSPR 247
DB 185 DVGACVAVLAVSVRYFKKCPFTVKNLAFPDTPV-MDSQSLVEVRGSCVNS3KE--EDPPR 241
QY 248 MHGSAEGEMLVPIGKCI CKAGYQOKGDTCPRCGRFVFKSSQDLQCRCP THSPSDEGS 307
DB 242 MYGSTEEMLVPIGKCTCNAGYERKGTICQACRPGFKASDGAACKCKCPHSHSTQDGS 301
QY 308 SRCECEDGYRAPSPDPYVACTRPSPAPONLIFININQTVSLSESPADN3GRNDVYR1 367
DB 302 MNCRCENNVFRAEKDPPSMACTRPSPAPRVVTSININETSVLDMSPWLDTGKRDIFNI 361
QY 368 LCKRCSEGECEVCPGCSNIGMPQOTGLEDNYTVMDLAHANTFEVEVNGVSDLSRS 427
DB 362 ICKKCGNNVQCEPCSPNVFELPQLGLTNTTYVVDLDAHNTYTFEIDVNVGSELSSP 421
QY 428 QRLFAAVSITTTGOAPSPQVSGVWKEERLQSVOLSWOEPHPKGVTEYIKYEEKORE 487
DB 422 PRQYAAVSITTTQAPSPVMTIKDRTSRNSISLSWEPHPHPIIUDYIKYEEKORE 481

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QY 488 RYSLTKSTKSTASINNLKRGTYVYFOIRAVTAAGYNSPRLDVATLEBASGMKEBATA 547
DB 482 TSYTILPARGTNTVITSLKPDITTYVFOIRAFRAAGYNSRKREFTSP-----DSFS 534
QY 548 VSESQNPVILIANVAVAGTIIIVFWPFGFLIRHCGYSKADQEGEE-LYF 598
DB 535 ISGENSHVMAISAAVAIVLT--VVTYVLVGRFGYHKSRSKSAEKKLHF 584

RESULT 14
EPA3_HUMAN STANDARD; PRT; 983 AA.
ID EPA3_HUMAN
AC P29320; Q9H2V3; Q9H2V4;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
kinase receptor ETK1) (HEK4).
GN Name=EPAH3; Synonyms=ETK, ETK1, HEK;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=92179233; PubMed=1311845;
RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine
kinase expressed by human lymphoid tumor cell lines";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Melanoma;
RX MEDLINE=20441582; PubMed=10987298;
RA Chiari R., Hames G., Stroobant V., Texier C., Maille B., Boon T.,
RA Coulle P.G.;
RT "Identification of a tumor-specific shared antigen derived from an Eph
receptor and presented to CD4 T cells on HLA class II molecules";
RL Cancer Res. 60:4855-4863(2000).
RN [3]
RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
RX MEDLINE=9217681; PubMed=1737782;
RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A.,
RA Welch K., Loudovaris M., Rockman S., Busmanis I.;
RT "Isolation and characterization of a novel receptor-type protein
tyrosine kinase (hek) from a human pre-B cell line.";
RL J. Biol. Chem. 267:3262-3267(1992).
RN [4]
RP SPLICED ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC - FUNCTION: Receptor for members of the ephrin-A family. Binds to
ephrin-A2, -A3, -A4 and -A5. Could play a role in lymphoid
function.
CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC - SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC - Secreted (isoform 2).
CC - ALTERNATIVE PRODUCTS:
-1- ALTERNATIVE SPLICING: Named isoforms=2;
Name=1;
IsoId=P29320-1; Sequence=displayed;
Note-May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=2;
IsoId=P29320-2; Sequence=VSP_002995, VSP_002996;
CC - TISSUE SPECIFICITY: Widely expressed. Highest level in placenta.
CC - SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
receptor subfamily.
CC - SIMILARITY: Contains 2 fibronectin type III domains.

```

CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M83941; AAA58633.1; -;
 DR EMBL; AF213459; AAG3576.1; -;
 DR EMBL; AF213460; AAG3577.1; -;
 DR EMBL; A28003; CAA01906.1; -;
 DR PIR; A38224; A38224;
 DR HSSP; P54763; IJPA;
 DR Genem; HGNC:3387; EPHA3.
 DR MIM; 179611; -;
 DR GO; GO:0005887; C:Integral to plasma membrane; TAS.
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003961; FN_III-like.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003962; FcII subd.
 DR InterPro; IPR008979; Gal bind like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; Ykase_receptor.
 DR Pfam; PF01404; Ephrin_1bd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPRIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS0853; FN3_2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW Alternative splicing; ATP-binding; Direct protein sequencing;
 KW Glycoprotein; Phosphorylation; Receptor; Repeat; Signal; Transferase;
 KW Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 20
 FT CHAIN 21 983 Ephrin type-A receptor 3.
 FT DOMAIN 21 541 Extracellular (Potential).
 FT TRANSMEM 542 565 Potential.
 FT DOMAIN 566 983 Cytoplasmic (Potential).
 FT DOMAIN 189 322 Cys-rich.
 FT DOMAIN 325 429 Fibronectin type-III 1.
 FT DOMAIN 437 528 Fibronectin type-III 2.
 FT DOMAIN 621 882 Protein kinase.
 FT DOMAIN 911 975 SAM.
 FT STR 981 983 PDZ-binding motif (Potential).
 FT NP_BIND 627 635 ATP (By similarity).
 FT BINDING 653 653 ATP (By similarity).
 FT ACT_SITE 746 746 By similarity.
 FT MOD_RES 596 596 Phosphotyrosine (by autocatalysis)
 FT MOD_RES 596 596 (Potential).
 FT MOD_RES 602 602 Phosphotyrosine (by autocatalysis)
 FT MOD_RES 602 602 (Potential).
 FT MOD_RES 779 779 Phosphotyrosine (by autocatalysis)
 FT MOD_RES 779 779 (Potential).

FT CARBOHYD 232 232 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 337 337 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 391 391 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 404 404 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 493 493 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 532 539 SPSISGS -> CWYFNVA (in isoform 2).
 FT VARSPLIC 540 983 /Ftrd=VSP_002995.
 FT VARSPLIC 540 983 Missing (in isoform 2).
 FT CONFLICT 507 507 F -> L (in Ref. 1; CAA01906).
 FT CONFLICT 724 724 V -> L (in Ref. 1; CAA01906).
 FT CONFLICT 911 911 S -> T (in Ref. 2).
 FT CONFLICT 924 924 R -> W (in Ref. 2).
 SQ SEQUENCE 983 AA; 110086 MW; B8D900FA80FF5121 CRC64;
 Query Match 53.8%; Score 1796; DB 1; Length 983;
 Best Local Similarity 57.6%; Pred. No. 1,7e-125;
 Matches 329; Conservative 102; Mismatches 128; Indels 12; Gaps 5;
 QY 28 QAAKEVLLDSKAQQTLEWISSPPSGMEISGLDENYTPRTYQVCQVNEPNNWMLRT 87
 DB 25 QPSNEVLLDSKTIQGLGMISSPHGMBEISGVDEHTPTRTYQVCNMDSQNNMLRT 84
 QY 88 NMISGNAORIFVBLKFTLRDQNSLPGLGTCKETFMILYYETDYGRIREMLVYKID 147
 DB 85 NMVPRNSAQKIYVBLKFTLRDQNSIPVLGTCKETFMILYYESDDHGVKREHQFTKID 144
 QY 148 TTADESFQGDLDGERCKKANTEVREIGPLSKKFPYLAPODVACIALYISKYYKKCWT 207
 DB 145 TTADESFQGDLDGERCKKANTEVREIGPLSKKFPYLAPODVACIALYISKYYKKCWT 204
 QY 208 IVENTLAVFPPTVTSSEFSSLVVGRGTVCSAEEBAENSPRHCSAEGEMLVPIGKICCKA 267
 DB 205 TVKNLAMPFDIVP-MDSQSLVEVSGCVNNSKE--EPPRYCTSGEMLVPIGKICCKA 261
 QY 268 GYQKQDTCPEPCGRPFYKSSODLQCSRPTSPSDESGRCEDEGYRAPSPDPYVA 327
 DB 262 GYERGFMCQACRGFPFKALDGNMKCAKCPHSHSTQSDGNNCCENNYFPADDPSPMA 321
 QY 328 CTRPPSAPONILFINOTTSLSEWSPADNGRNDVYTRILCKCSGEGECVCGSNIG 387
 DB 322 CTRPPSPPRNVISININETSIVLDMSPDLTGGRDVTFNIIICKKGNMKICGECSPNVR 381
 QY 388 YMPQQTGLEEDVYVWMLLAHANTFEVBAVNGVSDLSRSQRLPAVASITGQAPSPQVS 447
 DB 382 FLPRQGLTNTVTVTLAHTNTFEIDAIVNGVSELSPPROPAAVSITNQAAPEPVL 441
 QY 448 GVMKERYLQRSVQLSWQEPHPNGVITEIKYKEDQRETYSTLTKSTASINMLKP 507
 DB 442 TTKDRTSRNSISLSWQEPHPNGIILDEYKYEKQEGESTYTLIARGTNVTISLKP 501
 QY 508 GTTVVFPQIRAVTAAGYNGYSERLDVALTEASGCMFATAVSSQNPVIYIIAVAVAGTI 567
 DB 502 DTIVVFPQIRAVTAAGYNGYSEKPEFETSP-----DSFISGSSQVMIATSAVAI 554
 QY 568 ILVFMVGFIIIRHGHGYSKADQGDDELYF 598
 DB 555 LITVVIY-VLIG-RFCGYKSKGADKRLHF 583
 RESULT 15
 O6P4R6 PRELIMINARY; PRT; 983 AA.
 AC O6P4R6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE EPHA3 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]

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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 16.7136 Seconds
(without alignments) 3603.755 Million cell updates/sec

Title: US-10-073-064-5
Perfect score: 3338
Sequence: 1 MVVQTRPPSWILLCYWLLG.....DMEKTOHKKMKMIASCSRL 626

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

- 1: p1r1:*
- 2: p1r2:*
- 3: p1r3:*
- 4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3338	100.0	626	2 148614	developmental kina
2	3199	95.8	610	2 148612	developmental kina
3	3191	95.6	998	2 JC5672	receptor tyrosine
4	3159.5	94.7	605	2 JC5673	receptor tyrosine
5	3139	94.0	998	2 158351	receptor tyrosine
6	1841	55.2	991	2 178843	receptor protein-t
7	1834	54.9	981	2 S51604	receptor-like tyro
8	1819	54.5	1005	2 S49015	receptor tyrosine
9	1800	53.9	1013	2 150615	receptor-type prot
10	1796	53.8	983	2 A38224	receptor-tyrosine k
11	1790.5	53.6	985	2 151549	receptor-tyrosine k
12	1783.5	53.4	983	2 B45583	receptor tyrosine
13	1783.5	53.4	983	2 A45583	receptor tyrosine
14	1741.5	52.2	986	2 178844	receptor protein-t
15	1723	51.6	986	2 S78059	protein-tyrosine k
16	1655	49.6	948	2 S51605	receptor-like tyro
17	1498	44.9	995	2 A56599	embryo kinase 5 -
18	1467.5	44.0	970	2 178842	receptor protein-t
19	1449	43.4	984	2 A39753	protein-tyrosine k
20	1398	41.9	898	2 S47489	receptor tyrosine
21	1390	41.6	893	2 S51603	receptor-like tyro
22	1348	40.4	885	2 151672	receptor tyrosine
23	1335	40.0	849	2 150617	protein-tyrosine k
24	1276	38.2	988	2 150611	protein-tyrosine k
25	1273.5	38.2	982	2 S37627	protein-tyrosine k
26	1269.5	38.0	952	2 150612	protein-tyrosine k
27	1257	37.7	993	2 148653	mouse developmenta
28	1248.5	37.4	976	2 A36355	protein-tyrosine k
29	1231.5	36.9	877	2 148967	brain-specific kin

30	1199.5	35.9	977	2 S49004	tyrosine kinase Mp
31	1169	35.0	938	2 149071	protein kinase - m
32	1139.5	34.1	975	2 148974	receptor-protein t
33	1072.5	32.1	1006	2 JC5526	kinase-defective E
34	1064.5	31.9	984	2 A34076	protein-tyrosine k
35	1035.5	31.0	987	2 148652	mouse developmenta
36	1034	31.0	987	2 A54092	protein-tyrosine k
37	1022.5	30.6	987	2 148953	eph-related recept
38	784	23.5	1019	2 T13039	tyrosine kinase re
39	544	16.3	1122	2 T42400	Eph receptor tyros
40	382.5	11.5	919	2 T29581	hypothetical prote
41	362	10.8	612	2 S33506	protein-tyrosine k
42	251	7.5	87	2 C45583	receptor tyrosine
43	215.5	6.5	1232	2 T43027	neural cell adhesi
44	209	6.3	1436	2 JC5290	protein-tyrosine-p
45	206.5	6.2	1825	2 C88400	protein H19M22.1 l

ALIGNMENTS

RESULT 1

148614
developmental kinase 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 148614, S51742
R:Clonек, T.; Millaуer, B.; Ullrich, A.
Oncogene 9, 97-108, 1995
A:Title: Identification of alternatively spliced mRNA encoding variants of MDX1, a nove
A:Reference number: 148611
A:Accession: 148614
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-626 <RSS>
A:Cross-references: UNIPROT:Q61772; EMBL:X79084; NID:5607137; PIDN:CAA55689.1; PID:96071

Query Match	100.0%	Score 3338	DB 2	Length 626
Best local similarity	100.0%	Pred. No. 6.4e-233		
Matches 626	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MVVQTRPPSWILLCYWLLGFAHTGEAQAKEVLLDSKAQOTLEWISSPPSGMEISG	60	
DB	1	MVVQTRPPSWILLCYWLLGFAHTGEAQAKEVLLDSKAQOTLEWISSPPSGMEISG	60	
QY	61	LDENYTPIRTYQVQVMEPNQNMWLRNWSKGAQRIPELKTLLDQNSLPGVLTGCK	120	
DB	61	LDENYTPIRTYQVQVMEPNQNMWLRNWSKGAQRIPELKTLLDQNSLPGVLTGCK	120	
QY	121	ETFMUYETDYDGRNIRENLVYKIDTIADESFTQDGERKMKLNTREI:GPLSKK	180	
DB	121	ETFMUYETDYDGRNIRENLVYKIDTIADESFTQDGERKMKLNTREI:GPLSKK	180	
QY	181	GFYLAPODVAGACIALVSKVYKKKWTIVENLAVPPTVTGSEPSLVEVNGTCVSSAE	240	
DB	181	GFYLAPODVAGACIALVSKVYKKKWTIVENLAVPPTVTGSEPSLVEVNGTCVSSAE	240	
QY	241	EAENSPPMHGSAEEMLVPIGKCIKAGYQOGKPTCEPCGRFPYKSSODIQCRCPTHS	300	
DB	241	EAENSPPMHGSAEEMLVPIGKCIKAGYQOGKPTCEPCGRFPYKSSODIQCRCPTHS	300	
QY	301	FSDEGSSRCCEGGYRAPSDPYVACTRPPSAPOULIFINOTVTSLEMSPPADNGR	360	
DB	301	FSDEGSSRCCEGGYRAPSDPYVACTRPPSAPOULIFINOTVTSLEMSPPADNGR	360	
QY	361	NDVYTRILCKKCSWEGECVPCGSNIGMPQOTGLENDYVTMDLAAHYTFEAVNG	420	
DB	361	NDVYTRILCKKCSWEGECVPCGSNIGMPQOTGLENDYVTMDLAAHYTFEAVNG	420	
QY	421	VSDLSRGORLFAANSITTTGAAPSOVSWKERVLOQSVLSNPEPHNVCVITEYEIKY	480	
DB	421	VSDLSRGORLFAANSITTTGAAPSOVSWKERVLOQSVLSNPEPHNVCVITEYEIKY	480	

QY 481 YEKDQERTYSTLTKKSTASINNLKPGTYVFOIRAVTAAGYGNYPRLVATLEBASG 540
DB 481 YEKDQERTYSTLTKKSTASINNLKPGTYVFOIRAVTAAGYGNYPRLVATLEBASG 540
QY 541 KMEPATVSSSEONVITIAVAVAGTIIIVFMVGFIIIGRRHCGYSADQ3GDEBELYFHS 600
DB 541 KMEPATVSSSEONVITIAVAVAGTIIIVFMVGFIIIGRRHCGYSADQ3GDEBELYFHS 600
QY 601 LYRERGDMCKTQHNKKMTIASCSRL 626
DB 601 LYRERGDMCKTQHNKKMTIASCSRL 626

RESULT 2

148612
developmental kinase 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 148612; S51741
R/Closetek, T.; Millauner, B.; Ullrich, A.
Oncogene 9, 97-108, 1995
A>Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a novel
A:Reference number: 148611
A:Accession: 148612
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-610 <RES>
A/Cross-references: UNIPROT:Q61772; EMBL:X79083; NID:G607135; PION:CAA55688.1; PID:G60714

Query Match 95.8%; Score 3199; DB 2; Length 610;

Best Local Similarity 100.0%; Pred. No. 6, 6e-222;

Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVMQTRPSPWIIICYIMLGFATGGAQAQEVLLDLSKAQQTLEWISSPPSGMEISG 60
DB 1 MVMQTRPSPWIIICYIMLGFATGGAQAQEVLLDLSKAQQTLEWISSPPSGMEISG 60
QY 61 LDENYTPDIRTYQVCQVMEPNQNNMLRTNWSKNAQRI FVELKFTLRDQNSLPGLVGTCK 120
DB 61 LDENYTPDIRTYQVCQVMEPNQNNMLRTNWSKNAQRI FVELKFTLRDQNSLPGLVGTCK 120
QY 121 ETFNLVYETEDYDGTGNIRENLVYKIDTIAADESFTQGDIGERKMKLNTVEIREIGLSKK 180
DB 121 ETFNLVYETEDYDGTGNIRENLVYKIDTIAADESFTQGDIGERKMKLNTVEIREIGLSKK 180
QY 181 GFYLAPODVACIALVSVKYYKKCWITVENLA VFPDVTGSEFSSLVEVRGTCVSAAE 240
DB 181 GFYLAPODVACIALVSVKYYKKCWITVENLA VFPDVTGSEFSSLVEVRGTCVSAAE 240
QY 241 EAENSPPRMHCSAEGEWLVPIGKICICAKGYQOKGDTCEPCGRFRFYKSSODLQCSRPTHS 300
DB 241 EAENSPPRMHCSAEGEWLVPIGKICICAKGYQOKGDTCEPCGRFRFYKSSODLQCSRPTHS 300
QY 301 FSDREGSSRCECEGYYRAPSDDPYVACTRPPSAPQNLIFINQTTVLSLWSPADNGGR 360
DB 301 FSDREGSSRCECEGYYRAPSDDPYVACTRPPSAPQNLIFINQTTVLSLWSPADNGGR 360
QY 361 NDVTYRILICRCASWEGECVPCGSNIGMPQQTGLENNYTVNDLLAHAYTFEVLAVNG 420
DB 361 NDVTYRILICRCASWEGECVPCGSNIGMPQQTGLENNYTVNDLLAHAYTFEVLAVNG 420
QY 421 VSDLSRQRLFAAVSITTGQAAPQSVGVKMERVLQSRVLSWQEPHNPVITTEYIKY 480
DB 421 VSDLSRQRLFAAVSITTGQAAPQSVGVKMERVLQSRVLSWQEPHNPVITTEYIKY 480
QY 481 YEKDQERTYSTLTKKSTASINNLKPGTYVFOIRAVTAAGYGNYPRLVATLEBASG 540
DB 481 YEKDQERTYSTLTKKSTASINNLKPGTYVFOIRAVTAAGYGNYPRLVATLEBASG 540
QY 541 KMEPATVSSSEONVITIAVAVAGTIIIVFMVGFIIIGRRHCGYSADQ3GDEBELYFHS 600
DB 541 KMEPATVSSSEONVITIAVAVAGTIIIVFMVGFIIIGRRHCGYSADQ3GDEBELYFHS 600

QY 601 L 601
DB 601 L 601

RESULT 3

JC5672
receptor tyrosine kinase (BC 2.7.-.-) Etk precursor - mouse

N:Alternate names: developmental kinase 1

C:Species: Mus musculus (house mouse)

C>Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 09-Jul-2004

C/Accession: JC5672; I48611; S51740

R/Closetek, T.; Millauner, B.; Ullrich, A.

Oncogene 9, 97-108, 1995

A>Title: A novel truncated variant form of Etk/MDK1 receptor tyrosine kinase is expressed

A:Reference number: JC5672; MUID:98035156; PMID:9368721

A:Accession: JC5672

A:Molecule type: mRNA

A:Residues: 1-998 <TAL>

A/Cross-references: UNIPROT:Q61772

R/Closetek, T.; Millauner, B.; Ullrich, A.

Oncogene 9, 97-108, 1995

A>Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a novel

A:Reference number: 148611

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-998 <RES>

A/Cross-references: EMBL:X79082; NID:G607133; PION:CAA55687.1; PID:G607134

C/Comment: This enzyme plays a role during development involving differentiation and prol

C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat hc

C/Keywords: ATP; brain; phosphotransferase; transmembrane protein

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-998/Product: receptor tyrosine kinase Etk #status predicted <EXT>

F:31-553/Domain: extracellular #status predicted <EXT>

F:31-438/Domain: fibronectin type III repeat <FN1>

F:441-534/Domain: fibronectin type III repeat <FN2>

F:554-579/Domain: transmembrane #status predicted <TM>

F:611-697/Domain: protein kinase homology <KIN>

F:639-647/Region: protein kinase ATP-binding motif

F:920-986/Domain: SAM homology <SAM>

Query Match 95.6%; Score 3191; DB 2; Length 998;

Best Local Similarity 100.0%; Pred. No. 4, 8e-222;

Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVMQTRPSPWIIICYIMLGFATGGAQAQEVLLDLSKAQQTLEWISSPPSGMEISG 60
DB 1 MVMQTRPSPWIIICYIMLGFATGGAQAQEVLLDLSKAQQTLEWISSPPSGMEISG 60
QY 61 LDENYTPDIRTYQVCQVMEPNQNNMLRTNWSKNAQRI FVELKFTLRDQNSLPGLVGTCK 120
DB 61 LDENYTPDIRTYQVCQVMEPNQNNMLRTNWSKNAQRI FVELKFTLRDQNSLPGLVGTCK 120
QY 121 ETFNLVYETEDYDGTGNIRENLVYKIDTIAADESFTQGDIGERKMKLNTVEIREIGLSKK 180
DB 121 ETFNLVYETEDYDGTGNIRENLVYKIDTIAADESFTQGDIGERKMKLNTVEIREIGLSKK 180
QY 181 GFYLAPODVACIALVSVKYYKKCWITVENLA VFPDVTGSEFSSLVEVRGTCVSAAE 240
DB 181 GFYLAPODVACIALVSVKYYKKCWITVENLA VFPDVTGSEFSSLVEVRGTCVSAAE 240
QY 241 EAENSPPRMHCSAEGEWLVPIGKICICAKGYQOKGDTCEPCGRFRFYKSSODLQCSRPTHS 300
DB 241 EAENSPPRMHCSAEGEWLVPIGKICICAKGYQOKGDTCEPCGRFRFYKSSODLQCSRPTHS 300
QY 301 FSDREGSSRCECEGYYRAPSDDPYVACTRPPSAPQNLIFINQTTVLSLWSPADNGGR 360
DB 301 FSDREGSSRCECEGYYRAPSDDPYVACTRPPSAPQNLIFINQTTVLSLWSPADNGGR 360
QY 361 NDVTYRILICRCASWEGECVPCGSNIGMPQQTGLENNYTVNDLLAHAYTFEVLAVNG 420
DB 361 NDVTYRILICRCASWEGECVPCGSNIGMPQQTGLENNYTVNDLLAHAYTFEVLAVNG 420

Db 361 NDVTYRLICKRCSWEGECVPCGSNIGYMPQOTGLIEDNYVTVMDLAHANTFEVAVNG 420
Qy 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHNPVITEYEIKY 480
Db 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHNPVITEYEIKY 480
Qy 481 YEKQRERTYSTLTKTSTASINNLKPGTVVVFQIRAVTAAGYGNYSRPLDVATLEBASG 540
Db 481 YEKQRERTYSTLTKTSTASINNLKPGTVVVFQIRAVTAAGYGNYSRPLDVATLEBASG 540
Qy 541 KMFEATAVSSBQNPVITIIIAVAVAGTIIIVMVFQIIIGRRHCGYSKADQSGDEBELYPH 599
Db 541 KMFEATAVSSBQNPVITIIIAVAVAGTIIIVMVFQIIIGRRHCGYSKADQSGDEBELYPH 599

RESULT 4

JC5673
receptor tyrosine kinase (EC 2.7.-.-) Etk-ctd1 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 07-May-1999
C/Accession: JC5673
R/Author: A.H.; Muramatsu, T.; Kaneda, N.
Cell Struct. Funct. 22, 477-485, 1997
A/Title: A novel truncated variant form of EDK/MDK1 receptor tyrosine kinase is expressed
A/Reference number: JC5672; MUID:98035156; PMID:9368721
A/Accession: JC5673
A/Molecule type: mRNA
A/Residues: 1-605 <TAL>
A/Experimental source: embryo
C/Comment: This enzyme plays a regulatory role during neural development and embryogenesis
C/Keywords: brain; phosphotransferase
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-605/Product: receptor tyrosine kinase Etk-ctd1 #status predicted <MT>
F:31-546/Domain: extracellular #status predicted <EXT>
F:31-438/Domain: fibronectin type III repeat <FNI>
F:441-534/Domain: fibronectin type III repeat <FNI>
F:549-574/Domain: transmembrane #status predicted <TM>

Query Match 94.7%; Score 3159.5; DB 2; Length 605;
Best Local Similarity 99.2%; Pred. No. 4.6e-220;
Matches 596; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
Qy 1 MVVQTRPSPWIIICYLMLGFHTEGAQAQAKVLLDSKAQOTLEWISSPPSGMEISG 60
Db 1 MVVQTRPSPWIIICYLMLGFHTEGAQAQAKVLLDSKAQOTLEWISSPPSGMEISG 60
Qy 61 LDENVTPRTYQVCQVMEPNQNNMLRTNMISKGAQRIFVELKFTLRDQNSLPGVLTGCK 120
Db 61 LDENVTPRTYQVCQVMEPNQNNMLRTNMISKGAQRIFVELKFTLRDQNSLPGVLTGCK 120
Qy 121 ETFNLYYETDYGGRNIRENLVYKIDITIADESFQGDIGERKMKLNTVEIREIGPLSKK 180
Db 121 ETFNLYYETDYGGRNIRENLVYKIDITIADESFQGDIGERKMKLNTVEIREIGPLSKK 180
Qy 181 GFYLAFQDVGACIALVSKVYKKCMTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAE 240
Db 181 GFYLAFQDVGACIALVSKVYKKCMTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAE 240
Qy 241 EAENSPPRMHCSAEGEMVLVPIGKICIKAGYQKQKGTCEPCGRFPYKSSQDLQCSRCPHIS 300
Db 241 EAENSPPRMHCSAEGEMVLVPIGKICIKAGYQKQKGTCEPCGRFPYKSSQDLQCSRCPHIS 300
Qy 301 FSDREGSSRCCEGGRYRAPSDPPVACTRPPSAQNLIFFINQTTVLSLEMSPPADNGR 360
Db 301 FSDREGSSRCCEGGRYRAPSDPPVACTRPPSAQNLIFFINQTTVLSLEMSPPADNGR 360
Qy 361 NDVTYRLICKRCSWEGECVPCGSNIGYMPQOTGLIEDNYVTVMDLAHANTFEVAVNG 420
Db 361 NDVTYRLICKRCSWEGECVPCGSNIGYMPQOTGLIEDNYVTVMDLAHANTFEVAVNG 420
Qy 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHNPVITEYEIKY 480
Db 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHNPVITEYEIKY 480

Qy 481 YEKQRERTYSTLTKTSTASINNLKPGTVVVFQIRAVTAAGYGNYSRPLDVATLEBASG 540
Db 481 YEKQRERTYSTLTKTSTASINNLKPGTVVVFQIRAVTAAGYGNYSRPLDVATLEBASG 539
Qy 541 KMFEATAVSSBQNPVITIIIAVAVAGTIIIVMVFQIIIGRRHCGYSKADQSGDEBELYPH 600
Db 540 ----ATAVSSBQNPVITIIIAVAVAGTIIIVMVFQIIIGRRHCGYSKADQSGDEBELYPH 595
Qy 601 L 601
Db 596 L 596

RESULT 5

I58351
receptor protein-tyrosine kinase - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I58351
R/Fox, G.M.; Holte, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995
A/Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein-ty
A/Reference number: I58351; MUID:95206782; PMID:7898931
A/Accession: I58351
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-998 <RES>
A/Cross-references: UNIPROT:Q15375; GB:L36642; NID:9551607; PID:AAA74243.1; PID:9551608
A/Genes: HEK11
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C/Keywords: ATP; transmembrane protein
F:631-897/Domain: protein kinase homology <KTN>
F:639-647/Region: protein kinase ATP-binding motif
F:920-986/Domain: SAM homology <SAM>

Query Match 94.0%; Score 3139; DB 2; Length 998;
Best Local Similarity 97.7%; Pred. No. 2.7e-218;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MVVQTRPSPWIIICYLMLGFHTEGAQAQAKVLLDSKAQOTLEWISSPPSGMEISG 60
Db 1 MVVQTRPSPWIIICYLMLGFHTEGAQAQAKVLLDSKAQOTLEWISSPPSGMEISG 60
Qy 61 LDENVTPRTYQVCQVMEPNQNNMLRTNMISKGAQRIFVELKFTLRDQNSLPGVLTGCK 120
Db 61 LDENVTPRTYQVCQVMEPNQNNMLRTNMISKGAQRIFVELKFTLRDQNSLPGVLTGCK 120
Qy 121 ETFNLYYETDYGGRNIRENLVYKIDITIADESFQGDIGERKMKLNTVEIREIGPLSKK 180
Db 121 ETFNLYYETDYGGRNIRENLVYKIDITIADESFQGDIGERKMKLNTVEIREIGPLSKK 180
Qy 181 GFYLAFQDVGACIALVSKVYKKCMTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAE 240
Db 181 GFYLAFQDVGACIALVSKVYKKCMTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAE 240
Qy 241 EAENSPPRMHCSAEGEMVLVPIGKICIKAGYQKQKGTCEPCGRFPYKSSQDLQCSRCPHIS 300
Db 241 EAENSPPRMHCSAEGEMVLVPIGKICIKAGYQKQKGTCEPCGRFPYKSSQDLQCSRCPHIS 300
Qy 301 FSDREGSSRCCEGGRYRAPSDPPVACTRPPSAQNLIFFINQTTVLSLEMSPPADNGR 360
Db 301 FSDREGSSRCCEGGRYRAPSDPPVACTRPPSAQNLIFFINQTTVLSLEMSPPADNGR 360
Qy 361 NDVTYRLICKRCSWEGECVPCGSNIGYMPQOTGLIEDNYVTVMDLAHANTFEVAVNG 420
Db 361 NDVTYRLICKRCSWEGECVPCGSNIGYMPQOTGLIEDNYVTVMDLAHANTFEVAVNG 420
Qy 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHNPVITEYEIKY 480
Db 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHNPVITEYEIKY 480

Db 608 PEEBKMHEFN 617

RESULT 8

S49015

receptor tyrosine kinase Etk-1 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: S49015; S51602

R:Matsonpietere, P.C.; Barreuzeta, N.X.; Yancopoulos, G.D.

Oncogene 8, 3277-3288, 1993

A:Title: Etk-1 and Etk-2: two novel members of the Etk receptor-like tyrosine kinase family

A:Reference number: S49015; MUID:94067777; PMID:7504232

A:Accession: S49015

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1005 <MAI>

A:Cross-references: UNIPROT:P54757; EMBL:S68024

A:Note: the authors translated the codon GAC for residue 170 as Glu

A:Accession: S51602

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305, 'G', 359-1005 <MA2>

A:Cross-references: EMBL:S68026

A:Note: the authors translated the codon GAC for residue 170 as Glu

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h

C:Keywords: ATP; transmembrane protein

F:675-941/Domain: protein kinase homology <KIN>

F:663-691/Region: protein kinase ATP-binding motif

Query Match 54.5%; Score 1819; DB 2; Length 1005;

Best Local Similarity 55.1%; Pred. No. 4.9e-123;

Matches 348; Conservative 96; Mismatches 136; Indels 52; Gaps 10;

QY 6 RPEPMILLY-----IW---LIGFHTGEBAQAKEVLLDSKAQGTLEWISSPPSG 54

Db 25 RVPASLACGYASAPLKGPLMTCLLCAALRTLLASPSNEVNLDSRTVLGDLGWIAPFNG 84

QY 55 WEELSGIDENYTPRTVOVQVMEPNQNNMLRTNMISKGNQRIFEVEKFTLRDQNSLP 114

Db 85 WEELSGIDENYTPRTVOVQVMEPNQNNMLRTNMISKGNQRIFEVEKFTLRDQNSLP 144

QY 115 VLGTCKETFNLYYETDYDGTGRNIRENLVYKIDITIADESFTQDGERKKMLNTEVEEI 174

Db 145 GLGTCKETFNMYYESDDEGNIRKNDKQYIKIDITIADESFTQDGERKKMLNTEVEEI 204

QY 175 GPLSKGFFYLAFOVAGACIALVSVKYYKCKTIVENLAVFPDVTGSEFSSFLVEVRGTC 234

Db 205 GPLSKGFFYLAFOVAGACIALVSVKYYKCKTIVENLAVFPDVTGSEFSSFLVEVRGTC 264

QY 235 VSSAEBEENSPRMHCSAEGEWLVPGICIKAGYQKQDCEPCGRFFYSSQDLOCS 294

Db 265 VN--HSVTDPPKMHCSAEGEWLVPGICIKAGYQKQDCEPCGRFFYSSQDLOCS 322

QY 295 RCPHTSPDRSGSSRCEDEGYRAPSDPYVACTRPSPAPQNLIFINQTTVLSLEWSP 354

Db 323 KCPHSTHTEASISVCCEKDYFRRESPPFMACTRPPSAPRNALSNNEISVLEWLP 382

QY 355 ADNGRNDVYRIILCKRCSWEQECVPCGSGNIGYMPQGTGLEJNVYVMDLAAHANYFE 414

Db 383 ADTGCGKDVSYIILCKRCSWEQECVPCGSGNIGYMPQGTGLEJNVYVMDLAAHANYFE 442

QY 415 VEAANGVSDLSRQRLFAAVSITTCGAAPSOVSGMKEKRVLQRSVOLSMOEPHNGVIT 474

Db 443 IEANGVSDLSRQRLFAAVSITTCGAAPSOVSGMKEKRVLQRSVOLSMOEPHNGVIT 502

QY 475 EYEIKYEQQRERTYSLTKTSTASINNLKPGTVVYFOIRAYTAGYGYNSRLDVA 534

Db 503 EYEIKYEQQRERTYSLTKTSTASINNLKPGTVVYFOIRAYTAGYGYNSRLDVA 558

QY 535 LEEASGKMEATAY--SSSEONPVYIIIAVAVAGTIIIVFVFGFTI-----GRR- 581

Db 559 -----FETTPVFGASNDOSIPIIGSVTVGVIIAAVMI-GFLLSGSCCEGCGRAS 609

QY 582 -----HCGYSKADQDEGER-LYFHS 600

Db 610 SLCAVAHPSLIMRCGYSKAKODPEEKMHFFN 641

RESULT 9

150615

receptor-type protein-tyrosine kinase Cerk7, long splice form - chicken

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: 150615; 150616; 150614

R:Stiever, D.A.; Verderame, M.F.

Gene 148, 219-226, 1994

A:Title: Identification of a complete Cerk7 receptor protein tyrosine kinase coding sequence

A:Reference number: 150614; MUID:95047429; PMID:7958948

A:Accession: 150615

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1013 <SIB>

A:Cross-references: UNIPROT:P54755; EMBL:U03910; NID:9555617; PIDN:AA60612.1; PID:95556

A:Accession: 150616

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-572, 'R', 596-1013 <S12>

A:Cross-references: EMBL:U03910; NID:9555617; PIDN:AA60613.1; PID:9555619

A:Accession: 150614

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-279, 444-572, 'R', 596-1013 <S13>

A:Cross-references: EMBL:U03910; NID:9555617; PIDN:AA60614.1; PID:9555620

C:Genetics: Cerk7

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h

C:Keywords: alternative splicing; ATP; transmembrane protein

F:649-915/Domain: protein kinase homology <KIN>

F:657-665/Region: protein kinase ATP-binding motif

F:938-1004/Domain: SAM homology <SAM>

Query Match 53.9%; Score 1800; DB 2; Length 1013;

Best Local Similarity 55.7%; Pred. No. 1.2e-121;

Matches 345; Conservative 95; Mismatches 135; Indels 44; Gaps 9;

QY 8 PSM--IILCYTWLGFHTGEBAQAKEVLLDSKAQGTLEWISSPPSGEISGLDENY 65

Db 15 PSM--IILCYTWLGFHTGEBAQAKEVLLDSKAQGTLEWISSPPSGEISGLDENY 69

QY 66 TPRTVOVQVMEPNQNNMLRTNMISKGNQRIFEVEKFTLRDQNSLPGLVGTCKETFN 125

Db 70 TPRTVOVQVMEPNQNNMLRTNMISKGNQRIFEVEKFTLRDQNSLPGLVGTCKETFN 129

QY 126 YYETDYDGTGRNIRENLVYKIDITIADESFTQDGERKKMLNTEVEEI 185

Db 130 YYETDYDGTGRNIRENLVYKIDITIADESFTQDGERKKMLNTEVEEI 189

QY 186 FQVAGACIALVSVKYYKCKTIVENLAVFPDVTGSEFSSFLVEVRGTCV--SAEBAEN 244

Db 190 FQVAGACIALVSVKYYKCKTIVENLAVFPDVTGSEFSSFLVEVRGTCV--SAEBAEN 247

QY 245 SPRHCSAEGEWLVPGICIKAGYQKQDCEPCGRFFYSSQDLOCSRCPHTSPDR 304

Db 248 SPRHCSAEGEWLVPGICIKAGYQKQDCEPCGRFFYSSQDLOCSRCPHTSPDR 306

QY 305 EGSSRCECEGYTAPSDPYVACTRPSPAPQNLIFINQTTVLSLEWSP 364

Db 307 EGSSRCECEGYTAPSDPYVACTRPSPAPQNLIFINQTTVLSLEWSP 366

QY 365 YRIILCKRCSWEQECVPCGSGNIGYMPQGTGLEJNVYVMDLAAHANYFEVAVNGVSD 424

Db 367 YRIILCKRCSWEQECVPCGSGNIGYMPQGTGLEJNVYVMDLAAHANYFEVAVNGVSD 426

QY 425 SRQRLFAAVSITTCGAAPSOVSGMKEKRVLQRSVOLSMOEPHNGVITTEIKYKED 484

Db 427 NPGARQFVSVNVTNNQAPSPVSSVKKKITKNSISLSWQEPDRPNGLILEYEIKYFEKD 466
Qy 485 QRERTYSTLTKTSTASINNLKPGTVVYVFOIRAVTAAGYGNVSPRLDVATLEASGKMF 544
Db 487 Q-ETSYIIISKETAIRADGLKQGSAYVFOIRARTAGYGFGRREFEFT-----SP 537
Qy 545 ATAVSQNPVIIIAVAVAGTIIIVFMVFGPIIGRP-----H 562
Db 538 VLAASSDQSOIPII-VVSVTVGVILLAVIGFLLSGSCDCHGCGMASSLRPVAVPSLIWR 596
Qy 583 CGYSKADQEGDEE-LYFHS 600
Db 597 CGYSKAKQDPEEERKMFHN 615

RESULT 10

A38224
protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A38224; B38224
R/Wicks, J.P.; Wilkenson, D.; Salvaris, E.; Boyd, A.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
A/Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed
A/Reference number: A38224; MUID:92179233; PMID:1311845
A/Accession: A38224
A/Molecule type: mRNA
A/Residues: 1-983 <MTC>
A/Cross-references: UNIPROT:P29320; GB:M83941; NID:g183931; PID:AAA58633.1; PID:g183932
A/Experimental source: pre-B-cell leukemia cell line LK63
A/Note: sequence extracted from NCBI backbone (NCBI:P:86627)
A/Accession: B38224
A/Molecule type: protein
A/Residues: 21-39/810-860 <M12>
C/Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat
C/Keywords: ATP, autophosphorylation, glycoprotein, phosphoprotein, phosphotransferase,
F,1-20/Domain: signal sequence #status predicted <SIG>
F,21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
F,542-565/Domain: transmembrane #status predicted <TM>
F,619-685/Domain: protein kinase homology <KIN>
F,627-635/Region: protein kinase ATP-binding motif
F,232,337,391,404,493/Binding site: carboxylate (asn) (covalent) #status predicted

Query Match 53.8%; Score 1796; DB 2; Length 983;
Best Local Similarity 57.6%; Pred. No. 2,2e-121;
Matches 329; Conservative 102; Mismatches 128; Indels 12; Gaps 5;
Qy 28 QAAKEVLLDSKAQTELEWISSPPSGMERISGIDENYTPIRTYOVQVMEPNQNNMLRT 87
Db 25 QPSNEVNLDSKTIQGLGWIISYPSHGWEISGVDEHTPIRTYQVCNVMDHSGNNMLRT 84
Qy 88 NMISKGNARIFVELKFTLRDCNSLPVLTGCKETFMUYEETDYDGRIRRELYKID 147
Db 85 NMPVRNARQKIYELKFTLRDCNSIPVLTGCKETFMUYEESDDHDKGVAFREHGFKID 144
Qy 148 TIAADESFTQDGERMKKLNTEVREIGPLSKGFIYAFODVGACIALVSVKYYKKCWT 207
Db 145 TIAADESFTQMDLGRILKLNTEIREVGNPKKGFYLAFOVGCALVAVRVYFKKCP 204
Qy 208 IVENLAIFPTTVGSESSSLVEVGTGVSSAEEAEKSPRMHGAEEEMVPTGKICKA 267
Db 205 TVKNLAFPTTVP-MDSQSLVEVRGSCVNNKSKE--EDPPRYCSTEEBMLVPIGKSCNA 261
Qy 268 GYOQKGTCEPCGRFYFKSSSODLQCRPETHSPFDEGSSRCCEGEGYRAPSDPYVA 327
Db 262 GYERGMCAQCRGFFIKALDGNKCAKCPRHSTQDGSMMNCENNYRADDPSPMA 321
Qy 328 CTRPPSPQNLIFENINOTVLSLEWSPADNGGRNDVTYRILCKRCSMEQIECVPGSNIG 387
Db 322 CTRPPSPRNVISINETSIVLDSWPLDGTGRKDVTFNIIICKKCGNNIICCEPCSPNR 381
Qy 388 YMPQQTLEDNYVTVMLLAHANTFEVEAVNGVSDLSRSQRLPAAVSTTGQAAPQVS 447

Db 382 ELPRQGLNTVTYVTDLLAHNTYTEIDAIVNGVSELSPPPROFAAVSTTNQAPSPVL 441
Qy 448 GVAKERVLQRSVOLSWQEPHPNGVITEEIKYKEDQERTYSTLTKTSTASINNLKP 507
Db 442 TTKQDTSRNSISLSWQEPHPNGIILDEYKYEKQEOETSTILRAGTNTISSLR 501
Qy 508 GIVYVFOIRAVTAAGYGNVSPRLDVATLEASGKMFATVAVSQNPVIIIAVAVAGTI 567
Db 502 DTYVFOIRARTAGYGNVSRKREFETSP-----DSFISGSSQVVMIAIAVAAIL 554
Qy 568 IIVFMVFGPIIGRRHCGYSKADQEGDEELYE 598
Db 555 LITVVI-VLIG-RFCGYKSKGADKRLHF 583

RESULT 11

I51549
receptor tyrosine kinase - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I51549
R/Wimling, R.S.; Sargent, T.D.
Mol. Cell. Biol. 13, 219-229, 1994
A/Title: Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, has 1c
A/Reference number: I51549; MUID:95001564; PMID:7918105
A/Accession: I51549
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-985 <MIN>
A/Cross-references: UNIPROT:Q91694; GB:I26099; NID:g416402; PID:AAA64464.1; PID:g416403
A/Genetics:
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C/Keywords: ATP, transmembrane protein
F,618-884/Domain: protein kinase homology <KIN>
F,907-973/Domain: protein kinase ATP-binding motif
F,907-973/Domain: SAM homology <SAM>

Query Match 53.6%; Score 1790.5; DB 2; Length 985;
Best Local Similarity 55.5%; Pred. No. 5,4e-121;
Matches 347; Conservative 98; Mismatches 161; Indels 19; Gaps 7;
Qy 11 IILCIYWLGFATG-BAQAAKEVLLDSKAQTELEWISSP-PSGMEISGIDENYTP 68
Db 8 ILRCGFLGCAVATGSRIVPASVETLLDSVSGELGWIASPLSGMEISIMDEKNTPI 67
Qy 69 RTYOVQVMEPNQNNMLRTWISKGNARIFVELKFTLRDCNSLPVLTGCKETFMUYXX 128
Db 68 RTYOVQVMESSQNNMLRTDMIPRSGAKRYVEIKFTLRDCNSLPVMTGCKETFMUY 127
Qy 129 ETDYDGRIRRELYKIDTIAADESFTQDGERMKKLNTEVREIGPLSKGFIYAFOD 188
Db 128 ESNNDKRRFIRETOYKIDTIAADESFTQDIDGRIMKLNTEVREIGPLSKGFIYAFOD 187
Qy 189 VGACIALVSVKYYKKCWTIVENLAIFPTTVGSESSSLVEVGTGVSSAEEAEKSPRM 248
Db 188 VGACIALVSVRYKCCPLVRNLAQFPDTTSDSSSLVEVRGSCVNDSEK-KVVPKM 245
Qy 249 HGAEGEMLVPIKCIKCAKGYOQKGTCEPCGRFYFKSSSODLQCRPETHSPFDEGSS 308
Db 246 YCGADGEMLVPIKCIKCAKGYOQKGTCEPCGRFYFKSSSODLQCRPETHSPFDEGSS 305
Qy 309 RCEDEGYRAPSDPYVACTRPPSPQNLIFENINOTVLSLEWSPADNGGRNDVTYRIL 368
Db 306 SCICDRGYPADPDPSMPCTRPPSPQNLISVNETSVNLWESPNSSGPRDVSYNLV 365
Qy 369 CKRCSMEQIECVPGSNIGMPQQTLEDNYVTVMLLAHANTFEVEAVNGVSDLSRSQ 428
Db 366 CKRCSMDLTRCSPCGSGVHSPQONGIKTKTKYSINDLQAHNTYTFEVMALNGVSKNPEQ 425
Qy 429 RLFAAVSITTGQAAPQVSQVMEKERVLSVOLSWQEPHPNGVITEEIKYKEDQER 488
Db 426 DQAVSVTITNQAPSPVTVIOIPKXETIRHSVSLTWPPEPRANGVILEYKYEKQNER 485

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Qy 489 TSTLTKTSASINNLKPGTVVVFQIRAVTAAGYNSPRLDVATLLEASGKMFATAV 548
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 486 SYRIVKASASADJLGNLPLTGVFHVAKRTAGIGESGPEFTTNTVSPMIGEGT- 543
Qy 549 SSECNPVILIAVAVAGTIIIL-VEWVFGFIIGRRHCGYSKADQSGDEELVHSLYRERGD 607
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 544 ----SPYLL--VSAGSIVLVVILIAFAVISRRRSKSKAKQGEADEKHLNQGVTYVD 597
Qy 608 GMEKTQHNK-----KMMIASCRL 626
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 598 PFTYEDPNQAVREPAKEIDASCIRI 622

RESULT 12
B45583
C/Species: Gallus gallus (chicken)
C/Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B45583
R:Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol., 3, 769-778, 1991
A>Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
A/Reference number: A45583; MUID:92031278; PMID:1657122
A/Accession: B45583
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-983 <SAJ>
A/Cross-references: UNIPROT:P29318; GB:M68514; NID:9454809; PIDN:AAA48666.1; PID:G211447
A/Note: sequence extracted from NCBI backbone (NCBI:62405, NCBI:P:62411)
C/Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat h
C/Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif

Query Match 53.4%; Score 1783.5; DB 2; Length 983;
Best Local Similarity 57.7%; Pred. No. 1.7e-120;
Matches 340; Conservative 97; Mismatches 137; Indels 15; Gaps 7;

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Qy 11 IILCYIWLGPALHGEAOAAKEVLLDSKAQOLETEMISPPSGMEISGLDENYTPRT 70
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 LLLCA--ALSGAGRLSAPGNEVNLDSKTIQGEIGWISYSHGMEISGVDEHYTPRT 66
Qy 71 YQVCQWBNPNQNNMLRTNWSKGAORIFVELKFTLDCNSLPGVIGTCKETFNLYYT 130
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 YQSNVNDHSONNMLRTNWPNSAQKIYELKFTLDCNSIPVLGTCCKETFNLYTES 126
Qy 131 DYTGRNIRENLYVKIDITIADESFTQDGLGERMKLNTVEIREIGPLSKKGFYLAFOVG 190
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 DDHLAKFRHQFTKIDITIADESFTQMDLDRILKNTVEIREVGPVSKGFYLAFOVG 186
Qy 191 ACIALVSVKYYKCCMTIVENLAVPDTVTGSEFSSLVEVGTGVSSAEBAENSPRMHC 250
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 ACVALSVRYVFFKCCPFTVKNLAMPDTPV--MDSQSLVEVSGSCVNSKSE--EEDPKWYC 243
Qy 251 SAEEMLVPIGKICJCKAGYQOKGPTCEPCGRFRFYKSSQDLCRCRPHSHSDSEGSRRC 310
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 STEBEMLVPIGKICJCKAGYBERGFAQCRPGFTYASAGNVCACCPHSHSTYEDASLNC 303
Qy 311 ECEDEGYRAPSDPYVACTRPPSAPONLIFINNOTTVSLEWSPPADNGRNDVTYRIICK 370
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 RCEKNYFRSEKDPSPMACTRPPSAPRNVISINETSILDSWPLDTCGRDVTYRIICK 363
Qy 371 RCGSEQGECPVCGSNIGMPQOTGLIEDNYVTVMLLAHANTFEVEAVNGVSDLSRQRL 430
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 KCGSSSKICEPCSNVRFPLPRTGLTNTVTYVVDLHANTYTFEIDAVNGVSDLSRQ 423
Qy 431 FAASITTTGOAPSOVGVMKERVLORSVOLSMOEPEHPNVITEYEIKYEXKQREBTY 490
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 FAASITTTGOAPSPITVIRKDRSRNSVLSMOEPEHPNGIILDYEKTYEKQOQESTY 483
Qy 491 STLTKTSASINNLKPGTVVVFQIRAVTAAGYNSPRLDVATLLEASGKMFATAVSS 550
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 484 TILRAKSTNTVIGSLKEDDTTVVFQIRARTAAVYGTSSRKFEFTSP-----DSFSSS 536
Qy 551 EQNPVILIAVAVAGTIIILVPMVFGFIIGRRHCGYSKADQSGDEE-LYF 598
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 537 ENSQVMAISAAVAAILLTVVVY-VLIG-RFCGYKKSKEGTDEKRLHF 583

RESULT 13
A45583
C/Species: Mus musculus (house mouse)
C/Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A45583
R:Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol., 3, 769-778, 1991
A>Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
A/Reference number: A45583; MUID:92031278; PMID:1657122
A/Accession: A45583
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-983 <SAJ>
A/Cross-references: UNIPROT:P29319; GB:M68513; NID:9199119; PIDN:AAA39521.1; PID:9199120
A/Note: sequence extracted from NCBI backbone (NCBI:62398, NCBI:P:62401)
C/Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat h
C/Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif

Query Match 53.4%; Score 1783.5; DB 2; Length 983;
Best Local Similarity 56.4%; Pred. No. 1.7e-120;
Matches 334; Conservative 104; Mismatches 135; Indels 19; Gaps 8;

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Qy 13 LCYIWLGL---FATGE--AOAAKEVLLDSKAQOLETEMISPPSGMEISGLDENYTP 67
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 LSLIVLGGCCVLSGSGELSPQSPSNEVNLDSKTIQGEIGWISYSHGMEISGVDEHYTP 64
Qy 68 IRTYQVCWBNPNQNNMLRTNWSKGAORIFVELKFTLDCNSLPGVIGTCKETFNLYYT 127
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 IRTYQVCWBNPNQNNMLRTNWPNSAQKIYELKFTLDCNSIPVLGTCCKETFNLYYT 124
Qy 128 YETDYGRIRENLYVKIDITIADESFTQDGLGERMKLNTVEIREIGPLSKKGFYLAFO 187
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 MESD-DHGVFRFREQFTKIDITIADESFTQMDLDRILKNTVEIREVGPVSKGFYLAFO 183
Qy 188 DVGACIALVSVKYYKCCMTIVENLAVPDTVTGSEFSSLVEVGTGVSSAEBAENSPPR 247
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 DVGACIALVSVRYVFFKCCPFTVKNLAMPDTPV--MDSQSLVEVSGSCVNSKSE--EEDPPR 240
Qy 248 MHCAGEEMLVPIGKICJCKAGYQOKGPTCEPCGRFRFYKSSQDLCRCRPHSHSPSDEGS 307
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 MHCAGEEMLVPIGKICJCKAGYBERGFIQACRPGFTYASAGNVCACCPHSHSTYEDSGS 300
Qy 308 SRCEDEGYRAPSDPYVACTRPPSAPONLIFINNOTTVSLEWSPPADNGRNDVTYRI 367
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 MNCRCENNYFRAEKDPSPMACRPPSAPRNVISINETSILDSWPLDTCGRDITFNI 360
Qy 368 LCRGSEQGECPVCGSNIGMPQOTGLIEDNYVTVMLLAHANTFEVEAVNGVSDLSRS 427
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 361 ICCKCGNVNRCCEPCSNVRFPLPRTGLTNTVTYVVDLHANTYTFEIDAVNGVSELSSP 420
Qy 428 ORLFAVASITTTGOAPSOVGVMKERVLORSVOLSMOEPEHPNVITEYEIKYEXKQRE 487
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 421 PROFAVASITTTGOAPSPVWTIKKDRSRNSISLSMOEPEHPNGIILDYEKTYEKQOQ 480
Qy 488 RTYSLTKTSASINNLKPGTVVVFQIRAVTAAGYNSPRLDVATLLEASGKMFATAV 547
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 481 TSYTILRARGNTVIGSLKEDDTTVVFQIRARTAGYGTNSRKFEFTSP-----DSFS 533
Qy 548 VSSQNPVILIAVAVAGTIIILVPMVFGFIIGRRHCGYSKADQSGDEE-LYF 598
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 534 ISGENSHVMAISAAVAAILLT--VVTYVLVGRFCGYKKSKEGTDEKRLHF 583

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RESULT 14
178844
receptor protein-tyrosine kinase - human
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Jul-2004
C/Accession: 178844
R/Fox, G.M.; Holter, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995
A/Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty
A/Reference number: 158351; MUID:95206782; PMID:7898931
A/Accession: 178844
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-986 <RSS>
A/Cross-references: UNIPROT:P54764; GB:L36645; NID:G551613; PIDN:AAA74246.1; PID:G551614
C/Genetics:
A/Gene: HEK8
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
F/619-885/Domain: protein kinase homology <KIN>
F/908-974/Domain: SAM homology <SAM>

Query Match 52.2%; Score 1741.5; DB 2; Length 966;
Best Local Similarity 54.0%; Pred. No. 1.9e-117; Indels 19; Gaps 7;
Matches 327; Conservative 111; Mismatches 149;
QY 30 AKEVLLDSKAQQTLEWISSP-PSGMEISGLDENTYPTRYQVCQVMEINQNNMLRTN 88
DB 28 ANEVTLIDSRSVQGLGMIASPLEGMEVSIIMDEKPTIRTYQVCVMEHSQNNMLRTD 87
QY 89 WISGMGNQRIFFVELKFTLRQNSLPGLGCKTEFNYYETDPTGRNHNLYKIDT 148
DB 88 WITREGQRYVIEIKFTLRQNSLPVGMGCKTEFNYYESDDKRFHEQFVIDT 147
QY 149 IADDESFTQGLGERKKMLTEVEAIEIGLSKGFYLAFOVGAICALVSVYKKKWTI 208
DB 148 IADDESFTQGLGERKKMLTEVEAIEIGLSKGFYLAFOVGAICALVSVYKKKPLT 207
QY 209 VENIAVFPDVTGSEFSSSLVEVGTVCVSAEEAENSPRMHCASAEGLVYIGKCIKAG 268
DB 208 VRNIAQPPDITTGADTSLVEVRGSCVNNSEE--KDVPMKMGADGEMLVYIGNCLNAG 265
QY 269 YQKQGDTCPCGRFRFYSSSQDLCSCRCPHFSFSDREGSSRCEDGYVRAASPPRYAC 328
DB 266 HEERSGECQACKIGYVALSTDATCAKCPHYSVWEGATSCCTDRGPRADNDASMP 325
QY 329 TRPSAPQNLIFINQTTVSLSESPPADNGRNDVTYRIICKRC-SWEOG3CVFPCGSNIG 387
DB 326 TRPSAPNLINISNNETSVNLEWSSPQNTGRODISYNNVCKKCGADDPKCRFCSSGVH 385
QY 388 YMQQGTLEEDNYVTMDLHAHNTFFVEAVNGVDSLRSQRLFAAVSITTGQAAPSOVS 447
DB 386 YTPQONGLKTTKVYITDILAHNTYTFEIMAVNGVSKNPNPDGVSVTITNQAPSSIA 445
QY 448 GWMKERYLQSVQSNQPEHPHNGVITEYIKYKQKORERTYTLTKTSASINMLKP 507
DB 446 LVQAKETRYRSVALAMLEPKRPNGVILLEYEKYKQKQNSYKIVRTAARNTDIKLNP 505
QY 508 GTTVVFOIRAVTAAGYNSPRLDVATLEASGKMFATAVSSQONVILIAVAAGTII 567
DB 506 LITSVFHVRARTAGYGDPSLEPLVT-----NTVSRILIGDANSTVL--VSVGSV 557
QY 568 IL-VFMVFGITIGRHCGSKADQGDDELYFHSLYERKDGMEKTOHN-----KMTI 620
DB 558 VLVVILIAFAFVISRBRKSKAKQADBEKHLNGVRTYVDPFTYEDPNQAVREFAKEID 617
QY 621 ASCSRL 626
DB 618 ASCIKI 623

RESULT 15
S78059
protein-tyrosine kinase (EC 2.7.1.112) Eph precursor - mouse

C/Species: Mus musculus (house mouse)
C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: S78059; S30505; I58366
R/Charney, P.
submitted to the EMBL Data Library, March 1992
A/Reference number: S78059
A/Accession: S78059
A/Molecule type: mRNA
A/Residues: 1-986 <CHA>
A/Cross-references: UNIPROT:Q00137; EMBL:X65138; NID:G54083; PIDN:CAA6268.1; PID:G54084
R/Gillard-Hebenstreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chastier, A.; Wilkinson, Oncogene 7, 2499-2506, 1992
A/Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in ct
A/Reference number: S30496; MUID:93096484; PMID:1281307
A/Accession: S30505
A/Molecule type: mRNA
A/Residues: 1-31,55-986 <GIL>
A/Cross-references: EMBL:X65138
C/Genetics:
A/Gene: Sek
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C/Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase; t
F/1-15/Domain: signal sequence #status predicted <SIG>
F/1-986/Product: protein-tyrosine kinase Eph #status predicted <MAT>
F/348-569/Domain: transmembrane #status predicted <TM>
F/619-885/Domain: protein kinase homology <KIN>
F/627-635/Region: protein kinase ATP-binding motif
F/908-974/Domain: SAM homology <SAM>
F/235,340,408,423/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.6%; Score 1723; DB 2; Length 966;
Best Local Similarity 52.3%; Pred. No. 4e-116;
Matches 326; Conservative 117; Mismatches 162; Indels 20; Gaps 8;
QY 10 WITLCYTWLGFPAHTG-EAQAKVLLDSKAQQTLEWISSP-PSGMEISGLDENTYPT 67
DB 7 FILSPFLGICDAVTSRVRYPANEVTLIDRSRSQGLGMIASPLBEGMEVSIIMDEKNT 66
QY 68 IRTYQVCQVMEPNQNNMLRTNWSISKNAQRIFFVELKFTLRQNSLPGLGCKTEFNLY 127
DB 67 IRTYQVCVMEASQNNMLRTDWTIRBGAQGVYIEIKFTLRQNSLPVGMGCKTEFNLY 126
QY 128 YENDYDTGRNIRNLYKIDTILADESFTQGLGERKKMLTEVEAIEIGLSKGFYLAFO 167
DB 127 YESDNDKERIRFSQCKTDTILADESFTQVDIGDIMKMLTEIRVGPLSKGFYLAFO 166
QY 188 DVAGACIALVSVKYYKKKWTIYENIAVFPDVTGSEFSSSLVEVGTVCVSAEEAENS 247
DB 187 DVAGACIALVSVKYYKKKPLTYNLAQFPDITGADTSLVEVRGSCVNNSEE--KDV 244
QY 248 MHCSAGEMLVPIGKCIQKAGYQKADTCPCGRFRFYSSSQDLCSCRCPHFSFSDREGS 307
DB 245 MYCGADGEMLVPIGNCICNAHGEQNGEQAACKIGYKALSTDAKCAKCPHYSWEGA 304
QY 308 SRCEDEGYVRAASDPYVACTRPSAPQNLIFINQTTVSLSESPPADNGRNDVTYRI 367
DB 305 TSCCTCRGFFRANNDASMECTRPSPAPNLINISNNETSVNLEWSSPQNTGRODISY 364
QY 368 LCKRC-SWEOGECVPCGSNIGYMPQQTGLEDNVYTMDLHAHNTFFVEAVNGVDSL 426
DB 365 VCKKCGADPSKRPFGSGVHYTPQNGLKTTRVSTIDLLAHNTYTFEIMAVNGVSK 424
QY 427 SQRLFAVSLITGQAAPSOVSGVMKERYLQSVQSNQPEHPHNGVITEYIKYKQKOR 486
DB 425 SPDSVSVTVITNQAPSSIALVQAKETRYRSVALAMLEPKRPNGVILLEYEKYKQ 484
QY 487 ERTYSLTKTSSTASINMLKPGTVYVFOIRAVTAAGYNSPRLDVATLEASGKMEAT 546
DB 485 ERSYRIVRTAARTDIIKGLNPLITSYFHVHARARTAGGDFSEPLEVTT-----NTVPSR 538
QY 547 AVSSQONPVILIAVAAGTIIIL-VFMVFGITIGRHCGSKADQGDDELYFHSLYRER 605
DB 539 ITDQGANSTVLL--VSVGSVVLVILIAFAFVISRBRKSKAKQADBEKHLNGVRTY 596

Tue Aug 23 09:02:33 2005

us-10-073-064-5.rpr

Page 9

```

Oy      606 GDGMEKTQHNK-----KMWIASCSRL 626
          |      :      |      ||      :
Db      597 VDPFTYEDPNQAVREFAKEIDASCIRI 623

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Search completed: August 23, 2005, 08:33:12
Job time : 18.7136 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:30:14 ; Search time 112.437 Seconds
(without alignments)
2180.182 Million cell updates/sec

Title: US-10-073-064-5
Perfect score: 3338
Sequence: 1 MVVQTRPSPWILLCYWLLG.....DMEXTQHNKMKMTASCRL 626

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues
Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3191	95.6	998	10	US-09-823-187-42
2	3175	95.1	998	10	US-09-823-187-43
3	3139	94.0	945	15	US-10-112-944-260
4	3139	94.0	998	10	US-09-823-187-40
5	3031.5	90.8	993	10	US-09-823-187-39
6	3031.5	90.8	993	10	US-09-823-187-41
7	1841	55.2	991	10	US-09-823-187-44
8	1836.5	55.0	1041	18	US-10-840-512-215
9	1830.5	54.8	953	14	US-10-412-277-7
10	1827	54.7	991	17	US-10-732-923-13667
11	1819	54.5	1005	15	US-10-029-020-63

ALIGNMENTS

RESULT 1
US-09-823-187-42
; Sequence 42, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Gubey, Vladimir Y
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumar
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Patirajan, Meera
; APPLICANT: Shinkets, Richard A
; APPLICANT: Spaderna, Steven K
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier, Raymond J
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-745
; CURRENT APPLICATION NUMBER: US/09/823,187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/193,339
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/193,205
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/195,343
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,088
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,005
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,792
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/196,556
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/197,081

12	1817	54.4	1037	14	US-10-316-124-3	Sequence 3, Appli
13	1817	54.4	1037	15	US-10-353-690-40	Sequence 40, Appli
14	1817	54.4	1037	20	US-11-064-551-3	Sequence 3, Appli
15	1806.5	54.1	975	14	US-10-412-277-8	Sequence 8, Appli
16	1800	53.9	1013	17	US-10-732-923-13668	Sequence 13668, A
17	1796	53.8	666	9	US-09-771-161A-136	Sequence 136, App
18	1796	53.8	983	9	US-09-771-161A-227	Sequence 227, App
19	1796	53.8	983	14	US-10-205-823-97	Sequence 97, Appli
20	1796	53.8	983	14	US-10-345-680-2	Sequence 2, Appli
21	1796	53.8	983	15	US-10-295-027-602	Sequence 602, App
22	1796	53.8	983	15	US-10-029-020-59	Sequence 59, Appli
23	1796	53.8	983	17	US-10-794-514A-467	Sequence 467, App
24	1796	53.8	983	18	US-10-489-125B-11	Sequence 11, Appli
25	1790.5	53.6	985	15	US-10-029-020-61	Sequence 61, Appli
26	1783.5	53.4	968	14	US-10-412-277-6	Sequence 6, Appli
27	1783.5	53.4	983	17	US-10-732-923-13675	Sequence 13675, A
28	1741.5	52.2	921	9	US-09-805-020-52	Sequence 52, Appli
29	1741.5	52.2	986	16	US-10-723-860-597	Sequence 597, App
30	1734.5	52.0	1104	9	US-09-982-610-36	Sequence 36, Appli
31	1701.5	51.0	935	15	US-10-449-569-36	Sequence 36, Appli
32	1701.5	51.0	992	10	US-09-973-424A-5	Sequence 5, Appli
33	1701.5	51.0	992	10	US-09-973-424A-53	Sequence 53, Appli
34	1701.5	51.0	992	17	US-10-691-165-5	Sequence 5, Appli
35	1701.5	51.0	992	17	US-10-691-165-53	Sequence 53, Appli
36	1701.5	51.0	1005	15	US-10-449-569-2	Sequence 2, Appli
37	1701.5	51.0	1012	15	US-10-168-582-3	Sequence 34, Appli
38	1699.5	50.9	935	15	US-10-449-569-14	Sequence 52, Appli
39	1695	50.8	991	17	US-09-973-424A-52	Sequence 52, Appli
40	1695	50.8	991	17	US-10-691-165-52	Sequence 52, Appli
41	1671	50.1	1035	15	US-10-029-020-50	Sequence 20, Appli
42	1665.5	49.9	1036	10	US-09-971-708-2	Sequence 2, Appli
43	1665.5	49.9	1036	14	US-10-245-752-104	Sequence 104, App
44	1665.5	49.9	1036	14	US-10-245-859-104	Sequence 104, App
45	1665.5	49.9	1036	14	US-10-245-103-104	Sequence 104, App

;; PRIOR FILING DATE: 2000-04-13
;; PRIOR APPLICATION NUMBER: 60/197,525
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/197,087
;; PRIOR FILING DATE: 2000-04-14
;; NUMBER OF SEQ ID NOS: 103
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 42
;; LENGTH: 998
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-823-187-42

Query Match 95.6%; Score 3191; DB 10; Length 998;
Best Local Similarity 100.0%; Pred. No. 1,1e-243;

Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVOGTRPSPWIIILCYIWLGFAGTGEAQAQAEVLLDSKAQOTLEWISSPPSGWEEISG 60
DB 1 MVOGTRPSPWIIILCYIWLGFAGTGEAQAQAEVLLDSKAQOTLEWISSPPSGWEEISG 60
QY 61 LDENVTPRTYOVQVQWEPNOMNMLRTNWSKGAQRI FVELKFTLRDQNSLPGLGTCK 120
DB 61 LDENVTPRTYOVQVQWEPNOMNMLRTNWSKGAQRI FVELKFTLRDQNSLPGLGTCK 120
QY 121 ETFNLYYETDYGGRINRENLVYKIDTIADESFTQDGERKMKLNTVREIGPLSKK 180
DB 121 ETFNLYYETDYGGRINRENLVYKIDTIADESFTQDGERKMKLNTVREIGPLSKK 180
QY 181 GFYLAFOQVACIALVSKVYKKCWITVENLAVFPDVTGSEFSSLVE/RGTCVSSAAE 240
DB 181 GFYLAFOQVACIALVSKVYKKCWITVENLAVFPDVTGSEFSSLVE/RGTCVSSAAE 240
QY 241 EAENSPRMHGSAEGEWLVPVIGKCI CKAGYQOKGDTCEPCGRRFYKSSODLQCSRCPTHS 300
DB 241 EAENSPRMHGSAEGEWLVPVIGKCI CKAGYQOKGDTCEPCGRRFYKSSODLQCSRCPTHS 300
QY 301 FSDREGSRCECEGYRAPSDDPYVACTRPPSAQNLIFININOTVYSLWMSPPADNGR 360
DB 301 FSDREGSRCECEGYRAPSDDPYVACTRPPSAQNLIFININOTVYSLWMSPPADNGR 360
QY 361 NDVTYRILCKRCMSWEGECVPCGSNIGYMPQOTGLIEDNYVTVMDLAAHANTFEVEAVNG 420
DB 361 NDVTYRILCKRCMSWEGECVPCGSNIGYMPQOTGLIEDNYVTVMDLAAHANTFEVEAVNG 420
QY 421 VSDLSRQRLFAAVSITTTGAAPQVSGVMKERVLQRSVQLSWEPEHPNGVITEYEIKY 480
DB 421 VSDLSRQRLFAAVSITTTGAAPQVSGVMKERVLQRSVQLSWEPEHPNGVITEYEIKY 480
QY 481 YEKQRETTYSTLTKTSASINNLKPGTYVVFQIRAVTAAGYGNYSR.LDVATLEASG 540
DB 481 YEKQRETTYSTLTKTSASINNLKPGTYVVFQIRAVTAAGYGNYSR.LDVATLEASG 540
QY 541 KMFEATAVSSQNPVITIIAAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599
DB 541 KMFEATAVSSQNPVITIIAAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599

RESULT 2
US-09-823-187-43

;; Sequence 43, Application US/09823187
;; Publication No. US20030096952A1
;; GENERAL INFORMATION:

;; APPLICANT: Burgess, Catherine
;; APPLICANT: Gusev, Vladimir Y
;; APPLICANT: Liu, Xiaohong
;; APPLICANT: Majumder, Kumarud
;; APPLICANT: Padigaru, Muralidhar
;; APPLICANT: Paturajan, Meera
;; APPLICANT: Shimkera, Richard A
;; APPLICANT: Spaderna, Steven K
;; APPLICANT: Spytek, Kimberly
;; APPLICANT: Taupier, Raymond J

;; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;; FILE REFERENCE: 15966-745
;; CURRENT APPLICATION NUMBER: US/09/823,187
;; CURRENT FILING DATE: 2001-03-29

;; PRIOR APPLICATION NUMBER: 60/193,339
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: 60/193,205
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: 60/195,343
;; PRIOR FILING DATE: 2000-04-05
;; PRIOR APPLICATION NUMBER: 60/195,088
;; PRIOR FILING DATE: 2000-04-06
;; PRIOR APPLICATION NUMBER: 60/195,005
;; PRIOR FILING DATE: 2000-04-06
;; PRIOR APPLICATION NUMBER: 60/195,792
;; PRIOR FILING DATE: 2000-04-10
;; PRIOR APPLICATION NUMBER: 60/196,556
;; PRIOR FILING DATE: 2000-04-11
;; PRIOR APPLICATION NUMBER: 60/197,081
;; PRIOR FILING DATE: 2000-04-13
;; PRIOR APPLICATION NUMBER: 60/197,525
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/197,087
;; NUMBER OF SEQ ID NOS: 103
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 43
;; LENGTH: 998
;; TYPE: PRT
;; ORGANISM: Rattus norvegicus
US-09-823-187-43

Query Match 95.1%; Score 3175; DB 10; Length 998;
Best Local Similarity 99.2%; Pred. No. 2e-242;

Matches 594; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVOGTRPSPWIIILCYIWLGFAGTGEAQAQAEVLLDSKAQOTLEWISSPPSGWEEISG 60
DB 1 MVOGTRPSPWIIILCYIWLGFAGTGEAQAQAEVLLDSKAQOTLEWISSPPSGWEEISG 60
QY 61 LDENVTPRTYOVQVQWEPNOMNMLRTNWSKGAQRI FVELKFTLRDQNSLPGLGTCK 120
DB 61 LDENVTPRTYOVQVQWEPNOMNMLRTNWSKGAQRI FVELKFTLRDQNSLPGLGTCK 120
QY 121 ETFNLYYETDYGGRINRENLVYKIDTIADESFTQDGERKMKLNTVREIGPLSKK 180
DB 121 ETFNLYYETDYGGRINRENLVYKIDTIADESFTQDGERKMKLNTVREIGPLSKK 180
QY 181 GFYLAFOQVACIALVSKVYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
DB 181 GFYLAFOQVACIALVSKVYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
QY 241 EAENSPRMHGSAEGEWLVPVIGKCI CKAGYQOKGDTCEPCGRRFYKSSODLQCSRCPTHS 300
DB 241 EAENSPRMHGSAEGEWLVPVIGKCI CKAGYQOKGDTCEPCGRRFYKSSODLQCSRCPTHS 300
QY 301 FSDREGSRCECEGYRAPSDDPYVACTRPPSAQNLIFININOTVYSLWMSPPADNGR 360
DB 301 FSDREGSRCECEGYRAPSDDPYVACTRPPSAQNLIFININOTVYSLWMSPPADNGR 360
QY 361 NDVTYRILCKRCMSWEGECVPCGSNIGYMPQOTGLIEDNYVTVMDLAAHANTFEVEAVNG 420
DB 361 NDVTYRILCKRCMSWEGECVPCGSNIGYMPQOTGLIEDNYVTVMDLAAHANTFEVEAVNG 420
QY 421 VSDLSRQRLFAAVSITTTGAAPQVSGVMKERVLQRSVQLSWEPEHPNGVITEYEIKY 480
DB 421 VSDLSRQRLFAAVSITTTGAAPQVSGVMKERVLQRSVQLSWEPEHPNGVITEYEIKY 480
QY 481 YEKQRETTYSTLTKTSASINNLKPGTYVVFQIRAVTAAGYGNYSR.LDVATLEASG 540
DB 481 YEKQRETTYSTLTKTSASINNLKPGTYVVFQIRAVTAAGYGNYSR.LDVATLEASG 540
QY 541 KMFEATAVSSQNPVITIIAAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599

Db 541 KMFEATAVSSEQNPIIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDEBELYFH 599

RESULT 3
US-10-112-944-260
; Sequence 260, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Gezh
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pt_FL_genes Version 5.0
SEQ ID NO 260
LENGTH: 945
TYPE: PRT
ORGANISM: Homo sapiens
US-10-112-944-260

Query Match 94.0%; Score 3139; DB 15; Length 945;
Best Local Similarity 97.7%; Pred. No. 1.3e-239;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVTQRPSPMIIICVWLGFAHTGEOAKKAVLLDSKAQOTLEMISSPPSGWEEISG 60
DB 1 MVTQRPSPMIIICVWLGFAHTGEOAKKAVLLDSKAQOTLEMISSPPSGWEEISG 60
QY 61 LDENYPIRTYQVCQWEPNUNMLRTNWSKNAQRIFVELKFTLRDNCNLSGVLGTCK 120
DB 61 LDENYPIRTYQVCQWEPNUNMLRTNWSKNAQRIFVELKFTLRDNCNLSGVLGTCK 120
QY 121 EFTFNLYYETDVTGNIRENLYVKIDTAADESFTQGLGGERKMLNTEVEIRIGLSKK 180
DB 121 EFTFNLYYETDVTGNIRENLYVKIDTAADESFTQGLGGERKMLNTEVEIRIGLSKK 180
QY 181 GFYLAQDVGACIALSVKYYKCKWTIENLAVFPDVTGSEFSSILVEVGTGVSSABE 240
DB 181 GFYLAQDVGACIALSVKYYKCKWTIENLAVFPDVTGSEFSSILVEVGTGVSSABE 240
QY 241 EAENSRMHCASGEWLVPIGKICICAGYQOKGDTCEPCGRFRYKSSODLQCSRCPTHS 300
DB 241 EAENSRMHCASGEWLVPIGKICICAGYQOKGDTCEPCGRFRYKSSODLQCSRCPTHS 300

QY 301 FSDRGSSRCCEDEGYRAPSDPPVACTRPSAPQNLIFNINQTTVLSLEMSPPADNGCR 360
DB 301 FSDRGSSRCCEDEGYRAPSDPPVACTRPSAPQNLIFNINQTTVLSLEMSPPADNGCR 360

QY 361 NDVYRIILCKRCWQEGECVPCGSNIGYMPQOTGLEJNVTYMDLAAHANTFEVEAYNG 420
DB 361 NDVYRIILCKRCWQEGECVPCGSNIGYMPQOTGLEJNVTYMDLAAHANTFEVEAYNG 420

QY 421 VSDLSRSQRLFAFVITTTGOAAPSGVGMKERVQRSVQSWQEPHNGVITEYIKY 480
DB 421 VSDLSRSQRLFAFVITTTGOAAPSGVGMKERVQRSVQSWQEPHNGVITEYIKY 480

QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVVYFQIRAVTAAGYGNYSRLDVATLEBASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVVYFQIRAVTAAGYGNYSRLDVATLEBASG 540

QY 541 KMFEATAVSSEQNPIIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDEBELYFH 599
DB 541 KMFEATAVSSEQNPIIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDEBELYFH 599

RESULT 4
US-09-823-187-40
; Sequence 40, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:

APPLICANT: Burgess, Catherine
APPLICANT: Gusev, Vladimir Y
APPLICANT: Liu, Xiaohong
APPLICANT: Majumder, Kumarud
APPLICANT: Padigaru, Muralidhar
APPLICANT: Pattnajan, Meera
APPLICANT: Shinkets, Richard A
APPLICANT: Spaderma, Steven K
APPLICANT: Spytek, Kimberly
APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/823,187
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,081
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,525
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/197,087
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 998
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-187-40

Query Match 94.0%; Score 3139; DB 10; Length 998;
Best Local Similarity 97.7%; Pred. No. 1.4e-239;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

[illegible]

APPLICANT: Spytek, Kimberly
APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,081
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,525
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/197,087
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 993
TYPE: PRT
ORGANISM: Gallus gallus
US-09-823-187-41

Query Match 90.8%; Score 3031.5; DB 10; Length 993;
Best Local Similarity 94.5%; Pred. No. 4.7e-231;
Matches 566; Conservative 17; Mismatches 11; Indels 5; Gaps 1;

1 MVVORPSPWITLCYIMLGFAGTGEAOAKKEVLLDSKAQOQTELEWISSPSPGMEELISG 60
1 MVLRSRLPFWIMLGCWMLRFAHTGSAQAKKEVLLDSKAQOQTELEWISSPSPGMEELISG 60
61 LDENYPTRTYQVCCVMEBNONNMLRTNWSKGNQRLFEVLEKFTLRDCNSLPGVLTGCK 120
61 LDENYPTRTYQVCCVMEBNONNMLRTNWSKGNQRLFEVLEKFTLRDCNSLPGVLTGCK 120
121 EFTNLYYETDYDGTGRNIRENLYVKIDITIADESFQGDLSGRKKMLNTEVEIEGPLSKK 180
121 EFTNLYYETDYDGTGRNIRENLYVKIDITIADESFQGDLSGRKKMLNTEVEIEGPLSKK 180
181 GFYLAFOVGACIALVSVKVVYKKCKMTVENLAVFPDVTGSEFSLVEVRGTGVSSAE 240
181 GFYLAFOVGACIALVSVKVVYKKCKMTVENLAVFPDVTGSEFSLVEVRGTGVSSAE 240
241 EAENSPRMHCASAEGLVPIGKCIKAGYQKGDTCPEGRFRFYSSSODLQCSRCPTHS 300
241 EAENSPRMHCASAEGLVPIGKCIKAGYQKGDTCPEGRFRFYSSSODLQCSRCPTHS 300
301 FSDREGSSRCCEGDGYRAPSDPYVACTRPPSAQONLFININQTTVSLIEMSPADNGCR 360
301 FSDREGSSRCCEGDGYRAPSDPYVACTRPPSAQONLFININQTTVSLIEMSPADNGCR 360
361 FSDKSGSSRCDEDEYYRAPSDPYVACTRPPSAQONLFININQTTVSLIEMSPADNGCR 360
361 FSDKSGSSRCDEDEYYRAPSDPYVACTRPPSAQONLFININQTTVSLIEMSPADNGCR 360
421 VSDLSRQRLFAAASITTGQAAPSOVSGVMKERVLRQSVOLSWQEPHEHNGVITEYEIKY 480
421 VSDLSRQRLFAAASITTGQAAPSOVSGVMKERVLRQSVOLSWQEPHEHNGVITEYEIKY 480
481 YEKQDERTYSTLTAKTSSTASINNLKPGTVVYFQIRAVTAAAGYGYSPRLDVATTEASG 540
481 YEKQDERTYSTLTAKTSSTASINNLKPGTVVYFQIRAVTAAAGYGYSPRLDVATTEASG 540
541 YEKQDERTYSTLTAKTSSTASINNLKPGTVVYFQIRAVTAAAGYGYSPRLDVATTEASG 540
541 YEKQDERTYSTLTAKTSSTASINNLKPGTVVYFQIRAVTAAAGYGYSPRLDVATTEASG 540

541 KMFATAVSSSEONPIIIIAVAVAGTILVFMVFGFIIGRRHCGYSKADQGEDELYTH 599
540 -----ATAVSSSEONPIIIIAVAVAGTILVFMVFGFIIGRRHCGYSKADQGEDELYTH 594

RESULT 7
US-09-823-187-44
Sequence 44, Application US/09823187
Publication No. US20030096952A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine
APPLICANT: Gusev, Vladimir Y
APPLICANT: Liu, Xiaohong
APPLICANT: Majumder, Kundu
APPLICANT: Padigaru, Muralidhar
APPLICANT: Patnirajan, Meera
APPLICANT: Shinkels, Richard A
APPLICANT: Spaderna, Steven K
APPLICANT: Spytek, Kimberly
APPLICANT: Taupier, Raymond J

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,081
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,525
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/197,087
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 991
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-187-44

Query Match 55.2%; Score 1841; DB 10; Length 991;
Best Local Similarity 57.4%; Pred. No. 1.2e-136;
Matches 345; Conservative 97; Mismatches 133; Indels 26; Gaps 8;

6 RPPSW--IILCYIMLGFAGTGEAOAKKEVLLDSKAQOQTELEWISSPSPGMEELISG 63
6 RPPSW--IILCYIMLGFAGTGEAOAKKEVLLDSKAQOQTELEWISSPSPGMEELISG 63
13 RAPLWTCILLC-----AALRTILASPSNVEVNLDSRTYMGDLGWIAPKNGMEELGEAYDE 67
13 RAPLWTCILLC-----AALRTILASPSNVEVNLDSRTYMGDLGWIAPKNGMEELGEAYDE 67
64 NYTPRTYQVCCVMEBNONNMLRTNWSKGNQRLFEVLEKFTLRDCNSLPGVLTGCKETP 123
64 NYTPRTYQVCCVMEBNONNMLRTNWSKGNQRLFEVLEKFTLRDCNSLPGVLTGCKETP 123
128 NYAPLHTYQVCKVMEBNONNMLRTNWSKGNQRLFEVLEKFTLRDCNSLPGVLTGCKETP 127
128 NYAPLHTYQVCKVMEBNONNMLRTNWSKGNQRLFEVLEKFTLRDCNSLPGVLTGCKETP 127
124 NLVYETDYDGTGRNIRENLYVKIDITIADESFQGDLSGRKKMLNTEVEIEGPLSKG 183
124 NLVYETDYDGTGRNIRENLYVKIDITIADESFQGDLSGRKKMLNTEVEIEGPLSKG 183
184 LAFQDVGACIALVSVKVVYKKCKMTVENLAVFPDVTGSEFSLVEVRGTGVSSAEAEAE 243
184 LAFQDVGACIALVSVKVVYKKCKMTVENLAVFPDVTGSEFSLVEVRGTGVSSAEAEAE 243
243 LAFQDVGACIALVSVKVVYKKCKMTVENLAVFPDVTGSEFSLVEVRGTGVSSAEAEAE 243
243 LAFQDVGACIALVSVKVVYKKCKMTVENLAVFPDVTGSEFSLVEVRGTGVSSAEAEAE 243

Db 239 RPPSAPRNAISNVNITSVLEMI PPADTGRGDVSYLACKCKNSHAGCECGHVRVL 358
Qy 390 POOTLEJNDYVMDLLAHANTPEVEANVSDLSRSQRLFAAVSITGGAAPSOVGV 449
Db 339 PROGLKCTVSMVMDLAAHTNTTEIEAVNGVSDSPGARQYVAVVITNOAPSEVITV 418
Qy 450 MKERVLORSVLSWQEPHEHNGVITEYEIKYEKQDQERTYSTLKTSASINNLKPGT 509
Db 419 KKGKIAKNSISLSWQEPDRPNCIILEYEIKHFEKQD-ETSYTIKSKETITAEGLKPPAS 477
Qy 510 VYVFOIRAVTAAGYGNYSRDLVATLEASGKMFAT---AVSSEQNPVITIAVAVAGT 566
Db 478 VYVFOIRATAAGYGFSSRRFE-----FETTPVFAASDOSQIPVIAVSVTVG- 525
Qy 567 IILVFMVGFIIIGRRHCGSKADQESDE-LYFHS 600
Db 526 VILLAVIGVILSGRRCGYSKAKQDPEEKMHFN 560

RESULT 10

US-10-733-923-13667
; Sequence 13667, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgeton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO: 13667
; LENGTH: 991
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-733-923-13667

Query Match 54.7%; Score 1827; DB 17; Length 991;
Best Local Similarity 58.0%; Pred. No. 1.5e-135;
Matches 346; Conservative 95; Mismatches 134; Indels 22; Gaps 8;
Qy 8 PSM--IILCYWILGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSGMEISGLDENV 65
Db 15 PGMTCILLCALRLSLASPG-----SEVLLDSRTYMGDLGMIAYPKNGMEIIGVDENY 69
Qy 66 TEIRTYOVQVNEPNQNMRLRTNWSKGNARIFVELKFTLRDQNSLPGLGTCKETENL 125
Db 70 ARIHTYQVCKWQEQNMNMLTSMISNEGRPASSPFELKFTLRDQNSLPGLGTCKETENL 129
Qy 126 YYYEDYDTGRNIRENLVYKIDITIADESFTQDGLGERKMKLNTVEREIGPLSKGFYLA 185
Db 130 YFESDDEDEGRNIRENOYIKIDITIADESFTLELDGRVWKLNTVERDVGLTKKGFYLA 189
Qy 166 PDVACIALVAVKYKKCWITIVENTLAVPPTVVGSESSLVVRGTVS-SAEBAEN 244
Db 190 PDVGCIALVAVRYKKCPSVIRGLAFPPITITGADSSQLLEVSGLCVNHSVTDEA-- 247
Qy 245 SPRMCSAGEWLVPIGKICIKAGYQOKGDTCEPCGRFRFYKSSODLQCSRPTHSFSDR 304
Db 248 -PKMCSAGEWLVPIGKLCAGYBEKNTQCVCRPGFKASPHSPSCSKPPHSYTLTD 306
Qy 305 EGSRSCEGEGYRRAPSDPPYACTRPPAPQNLFINIQTVLSLWSPAPANGGRNDYT 364
Db 307 EASTCLCEHYFRRESDDPTWACTRPPAPSAISNVNITSVLEMI PPADTGRGDVSYL 366
Qy 365 YAILCRGSEWQEGECPVCSNIGVMPQOTGLENDYVMDLLAHANTPEVEANVSDLS 424
Db 367 YIACKCKSHSGLCACGSHVRYLPQOGLKNTSVMMDLAAHTNTTEIEAVNGVSDQ 426
Qy 425 SRSORLFAAVSITGGAAPSOVGVWKEKRLORSVLSWQEPHEHNGVITEYEIKYEKQ 484

Db 427 NPGARQVSVVNTNOAPSPSVSVYKCKITKNSISLSWQEPDRPNCIILEYEIKYFEKD 486
Qy 485 QERTYSTLKTSASINNLKPGTVYFQIRAVTAAGYGNYSRDLVATLEASGKAFE 544
Db 487 Q-ETSYTIKSKETITAEGLKPPASVYFQIRARAAGYGFSSRRFEET-----SP 537
Qy 545 ATAVSSEQNPVITIAVAVAGTIIIVFVFGIIGRRHCGYSKADQESDE-LYFHS 600
Db 538 VLAASDQSQPII-VSVTVGILLAVVIGFLLSGRRCGYSKAKQDPEEKMHFN 593

RESULT 11

US-10-029-020-63
; Sequence 63, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangoli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 63
; LENGTH: 1005
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-029-020-63

Query Match 54.5%; Score 1819; DB 15; Length 1005;
Best Local Similarity 55.1%; Pred. No. 6.6e-135;
Matches 348; Conservative 96; Mismatches 136; Indels 52; Gaps 10;
Qy 6 RPPSMIILCY-----IWL---LIGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSG 54
Db 25 RVPASLACYSAPLKGPIMLTCLLCALRLTSLASPSNVNLLDSRTVLDGLGMAFPNG 84
Qy 55 WEISGLDENVTPRTYOVQVNEPNQNMRLRTNWSKGNARIFVELKFTLRDQNSLP 114
Db 85 WEISEVDENTAIPHTYOVCKWQEQNMNMLTSMISNEGRPASSPFELKFTLRDQNSLP 144
Qy 115 VLGTCKETENLYYYEDYDTGRNIRENLVYKIDITIADESFTQDGLGERKMKLNTVERE 174
Db 145 GIGTCKETENLYYYEDSDENGNIKDNOYIKIDITIADESFTLELDGRVWKLNTVERDV 204
Qy 175 GPLSKGYYLAFQDYGACIALVAVKYKKCWITIVENTLAVPPTVVGSESSLVVRGTC 234
Db 205 GPLSKGYYLAFQDYGACIALVAVRYKKCPSVIRGLAFPPITITGADSSQLLEVSGLC 264
Qy 235 VSSAEEBAENSPRMCSAGEWLVPIGKICIKAGYQOKGDTCEPCGRFRFYKSSODLQCS 294
Db 265 VM--HSTVDDEPKMCSAGEWLVPIGKCKAGYBEKNTQCVCRPGFKASPHSQC 322
Qy 295 RCPTHSFDRGSSRCEGEGYRRAPSDPPYACTRPPAPQNLFINIQTVLSLWSP 354

Db 323 KCPHSTHHEASTSCVCEKDYFRRESPPPTMACTRPPSAPRNAISVNTSVLEMTIP 382
Qy 355 ADNGRNDVYRIILCKRCSWEGECVPCGSNIYMPQOTGLEJNYVTMDLHANYTE 414
Db 363 ADTGCKGVSYIILCKKCNHSHAGVCECGHVRYPQDILKNTSVWMAADPLAHNTYFE 442
Qy 415 VEAVNGVDSLRSQSLFPAVSTTTGOAAPSOVSGMKERVLORSVQLSWOEPHPNGYIT 474
Db 443 IEAVNGVDSLPGTQYVSVNTTQOAPSPVTNNKKKIAKNSISLSWOEPDRNGIIL 502
Qy 475 EYEIYVYKEDORERTYSTLKTSTASINNLKPGVYVFOIRAVTAAGVNSPRLDVAT 534
Db 503 EYEIYVYKEDQ EISYTIILKSKETITTAAGLKPASVYVFOIRARTAGVYFSRRFE 558
Qy 535 LEBASGKMEATAV---SSEQNPVILIAVAVAGTIIIVFWGFIIL-----GRR- 581
Db 559 -----FETTPVGAANDSQPIILIGSVTVGVIILAVMI-GLLSGS3CECGCGRAS 609
Qy 582 -----HCGYSKADDEGDEE-LYFHS 600
Db 610 SLCAVAHPSLIWRCGYSKAKODPEEEKMHFNH 641

RESULT 12
US-10-316-124-3
; Sequence 3, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
; FILE REFERENCE: MP101-291P1RM
; CURRENT APPLICATION NUMBER: US/10/316,124
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-316-124-3

Query Match 54.4%; Score 1817; DB 14; Length 1037;
Best Local Similarity 55.5%; Pred. No. 1e-134;
Matches 346; Conservative 97; Mismatches 132; Indels 48; Gaps 10;

Qy 6 RPPSW--ILCYIMLGFAGTGEAQAKEVLLDSKAQOTELEWISSPPSGMEETISGLDE 63
Db 37 RAPLWTCLLC-----AALRTILASPSNEVNLDSRTVGDGLGWIAPKNGWEEIGEVDE 91
Qy 64 NYTPRTYOVQVQWEPNOMNMLRTWISKNAQRIFVFLAKTILRDNSL3VLTGCKETTF 123
Db 92 NYAPHTYQVCKWEMQONNMMLTSMISNEGSRIFELKFTLRDQNSL3GLGCKETTF 151
Qy 124 NLUYETDYDGRNRIRENLYVYKIDITIADESFQDGLGERMKKNTETVRJIGPLSKGFY 183
Db 152 NMUYTESDQNGRNIRKENQYIKIDITIADESFTELDLDRWKLNTETVRJYVGLSKGFY 211
Qy 184 LAFQDVGAICIALVSVYVYKCKWTIVENLAVFPDITVTSSEFSSLVEVRGTCVSSAEEBAE 243
Db 212 LAFQDVGAICIALVSVYVYKCKPSVVRHLAVFPDITVTSSEFSSLVEVRGTCVSSAEEBAE 269
Qy 244 NSPRMHGAEGBMLVPIKCLCKAGYQOKGDTCEPCGGRFVYKSSQDLC3RCPHHSDD 303
Db 270 EPPKMHGAEGBMLVPIKCMCKAGYEBKNGTCVCRGFPKASPHIOS3CKCPHSTYTH 329
Qy 304 REGSRCECEGQYVAPSDPVPYVACTRPPSAPONLIIFINOTTVLEWS3PADNGGRNDV 363
Db 330 EEAISTCVCEKDYFRRESPPPTMACTRPPSAPRNAISVNTSVLEMTIPADTGGRKDV 389

Qy 364 TYRILCKRCSWEGECVPCGSNIYMPQOTGLEJNYVTMDLHANYTEVEAVNGVSD 423
Db 390 SYTLACKKCNHSHAGVCECGHVRYPQDILKNTSVWMAADPLAHNTYFEIEAVNGSD 449
Qy 424 LSRGQPLFAAVSITTTGOAAPSOVSGMKERVLORSVQLSWOEPHPNGVITEYIKYEEK 483
Db 450 LSPGARQVSVNVTNQAAPSPVTNNKKKIAKNSISLSWOEPDRNGIILEYIKKPEK 509
Qy 484 DORERTYSTLKTSTASINNLKPGVYVFOIRAVTAAGVNSPRLDVATLEBASGMF 543
Db 510 DQ-ETSYTIILKSKETITTAAGLKPASVYVFOIRARTAGVYFSRRFE-----F 557
Qy 544 EAT---AVSQNPVILIAVAVAGTIIIVFWGFIIL-----GRR----- 581
Db 558 ETTVPFAASSDQSGIPIAVSVTVG-VIILAVTVGVIILSGSCBCCGCGRASLCAVAHPI 616
Qy 582 ---HCGYSKADDEGDEE-LYFHS 600
Db 617 LIWRCGYSKAKODPEEEKMHFNH 639

RESULT 13
US-10-353-690-40
; Sequence 40, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Accion, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Rodrique-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 9812, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; FILE REFERENCE: MP102-018P1RNMNMIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 1037
; TYPE: PRT


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0Y 30 KAEVLLLSKAOQTELEMTSSPPSGEETISGDENTPEIRYQVOCVMEP:QNNMT:RTNM 89
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 SNEVLLBSKRYMGDLGWIAPFKNGHEE:IGVDENYAP:HHYQVCKMYEQ:QNNMT:LTSH 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 90 ISKGNAB:IFEVLKFTLRDCNS:PGVLGTCKET:FNLYYYETDYDTRNT:RNNLYKIDTT 149
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 ISNEGAS:IFIELKFTLRDCNS:PGGLGTCKET:FNMYFESPDQNNR:IKENY:KIDTT 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 150 AADESFOTGD:GERKMK:NTREYRE:IGPLSKKPYLA:FOVGACIAL:VSK:YYKKCWITLY 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 AADESFTELJD:GDWRK:NTREYVDG:PLSKKGYLA:FOVGACIAL:VSR:YYKKCP:SVV 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 210 ENIAF:PPVTVTSSEFSL:VEYRGTCYSSAEEEAENS:PRMHC:SAEGEWLP:IGKCI:CKAGY 269
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 RHLAF:PDITTCADSSQLLEVS:GCYN --HSTYDPEPKHC:SAEGEWLP:IGKCM:CKAGY 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 270 QOKGDTCPECGRR:FYKSSSQDQCSRCP:HTSPFSDBRGSRC:CEDEGY:YRA:PSDP:PVYACT 329
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 229 EEKNTQCVCRG:GFPKASPH:IGSCGKCP:PHSYTHEAS:TSVCYCEKDY:FRFR:3SDP:PTMAC 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 330 RPPSA:PNULFIN:NOTTYSLEWS:PPADNGGRNDVY:RIILCKRCSWQEGECVP:CGS:INIGM 389
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 RPPSA:PRNAISVN:NETSVLEW:IPADDTGRKDVSY:IIACKKCN:SAAGVC:EECGGH:RYL 358
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 390 PQGTLENNYVVM:LLAHANTFEYEA:NGVSDLSRQRLFA:VSIITGGAASQV:SGV 449
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 359 PRQSLKNTISVMW:VDL:LAHTNTYFELEA:NGVSDLS:PGARQYVAVV:TNNAAPS:PV:TNV 418
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 450 MKER:LOBSVOL:SWOPE:HEPNVITEYE:IKYVEKQDREKTY:STLTKT:STAS:INNLK:PGT 509
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 419 KKGK:IAKKS:ISL:SWQED:PRPN:GILLEYELKH:EKQD --E:SYTI:IKSKET:ITL:MEGLK:PS 477
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 510 VYVFOIRAVTAAGY:NGYSPRLDVA:ILTEASGKM:FEAT --AVSSBONPV:IIIAVVA:VAGT 566
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 478 VYVFOIR:ARTAGYGVFSRRFE -----FETTPVFA:SSDQSL:FI:VIAV:STVG- 525
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 567 IILVFMV:GFIL -----GRR -----HCGYSKADQ:DEGEE --LYEHS 600
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 526 VILLAV:VIGVLLSGSC:CECGCRASSLCAV:AHPIILIRCGYS:IAKQDPEE:EKHFFIN 582

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Job time : 114.937 secs

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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 21.7783 Seconds
(without alignments)
2145.727 Million cell updates/sec

Title: US-10-073-064-5
Perfect score: 3338
Sequence: 1 MVVQTRPPSWIILCYWILG.....DMEKTOHKKMIAASCSRL 626

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*\n2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*\n3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*\n4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*\n5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*\n6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3338	100.0	626	3	US-08-368-776A-5
2	3338	100.0	626	3	PCT-US96-00419-5
3	3199	95.8	610	3	US-08-368-776A-3
4	3199	95.8	610	3	PCT-US96-00419-3
5	3191.5	95.6	994	3	US-08-368-776A-12
6	3191	95.6	998	3	US-08-368-776A-2
7	3191	95.6	998	3	PCT-US96-00419-2
8	3151.5	94.4	993	3	US-08-368-776A-11
9	3139	94.0	998	2	US-08-449-645A-17
10	3139	94.0	998	2	US-08-702-367A-17
11	3139	94.0	998	4	US-09-949-016-6501
12	3139	94.0	998	5	PCT-US95-04681-17
13	3139	94.0	1005	4	US-09-949-016-9901
14	1841	55.2	991	2	US-08-449-645A-13
15	1841	55.2	991	2	US-08-702-367A-13
16	1841	55.2	991	5	PCT-US95-04681-13
17	1833.5	54.9	967	2	US-08-449-645A-30
18	1833.5	54.9	967	2	US-08-702-367A-30
19	1830.5	54.8	953	4	US-09-751-389-7
20	1822	54.6	1005	4	US-08-469-537A-103
21	1806.5	54.1	975	4	US-09-751-389-8
22	1790	53.6	983	1	US-08-167-919A-10
23	1790	53.6	983	2	US-08-449-645A-21
24	1790	53.6	983	2	US-08-702-367A-21
25	1790	53.6	983	3	US-08-715-106-10
26	1790	53.6	983	4	US-09-442-649-10
27	1790	53.6	983	5	PCT-US95-04681-21

28 1783.5 53.4 968 4 US-09-751-389-6
29 1776 53.2 982 2 US-08-673-789-4
30 1775.5 53.2 983 1 US-08-162-809-16
31 1741.5 52.2 986 2 US-08-449-645A-15
32 1741.5 52.2 986 2 US-08-702-367A-15
33 1741.5 52.2 986 5 PCT-US95-04681-15
34 1741.5 52.0 997 4 US-09-949-016-7171
35 1734.5 52.0 1104 1 US-08-222-616-36
36 1734.5 52.0 1104 3 US-08-446-648-36
37 1734.5 52.0 1104 4 US-09-982-610-36
38 1734.5 52.0 1104 5 PCT-US95-04228-36
39 1734 51.9 986 2 US-08-673-789-3
40 1701.5 51.0 1005 4 US-09-949-016-6968
41 1701.5 51.0 1005 4 US-09-949-016-10620
42 1665.5 49.9 1036 4 US-09-751-389-2
43 1661.5 49.8 942 4 US-10-004-542-2
44 1661.5 49.8 942 4 US-10-430-797-2
45 1655 49.6 948 2 US-08-469-537A-101

ALIGNMENTS

RESULT 1
US-08-368-776A-5
Sequence 5, Application US/08368776A
Patent No. 6306482
GENERAL INFORMATION:
APPLICANT: Closser, Thomas
APPLICANT: Ullrich, Axel
APPLICANT: Millaer, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF MDK1
TITLE OF INVENTION: SIGNAL TRANSDUCTION
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368, 776A
FILING DATE: January 3, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 626 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-368-776A-5

Query Match 100.0%; Score 3338; DB 3; Length 626;
Best Local Similarity 100.0%; Pred. No. 1.3e-298;
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVTQRFPSWIIICYLWLGFAHTGEAQAKEYLLDLSKAQTELEWISSPPSGMEISG 60
    |||
DB 1 MVTQRFPSWIIICYLWLGFAHTGEAQAKEYLLDLSKAQTELEWISSPPSGMEISG 60
QY 61 LDENYPIRTYQVCQVMEPNQNNWLRTNWSKGNARIFVELKFTLRDNCNLSLPGVLTCK 120
    |||
DB 61 LDENYPIRTYQVCQVMEPNQNNWLRTNWSKGNARIFVELKFTLRDNCNLSLPGVLTCK 120
QY 121 EFTNLYYYETDYDTGGRNIRENLVYKIDTIADESFTQDGLGERKMKLNTVEIRIGPLSKK 180
    |||
DB 121 EFTNLYYYETDYDTGGRNIRENLVYKIDTIADESFTQDGLGERKMKLNTVEIRIGPLSKK 180
QY 181 GFYLAFODVACIALVSVKYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
    |||
DB 181 GFYLAFODVACIALVSVKYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPRMCSAAGEWLVPIGKICIKAGYQOKGDTCEPCGRRTYKSSSDLOCSRCPHIS 300
    |||
DB 241 EAENSPPRMCSAAGEWLVPIGKICIKAGYQOKGDTCEPCGRRTYKSSSDLOCSRCPHIS 300
QY 301 FSDREGSSRCECEDGYRRASDPDYVACTRPPSAPQNLIFINQTTVLSLEWSPADNGR 360
    |||
DB 301 FSDREGSSRCECEDGYRRASDPDYVACTRPPSAPQNLIFINQTTVLSLEWSPADNGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQGTGLENDYVTMDLAAHANYTEVEAVNG 420
    |||
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQGTGLENDYVTMDLAAHANYTEVEAVNG 420
QY 421 VSDLSRQRLFAAVSTTTGQAAPSOVSQVWKERYLQRSVOLSQOEPHHPGVITTEYIKY 480
    |||
DB 421 VSDLSRQRLFAAVSTTTGQAAPSOVSQVWKERYLQRSVOLSQOEPHHPGVITTEYIKY 480
QY 481 YEKDQERRTYTLTKTSTASINNLKPGTYVYFOIRAVTAAGYGNVSPRLDVAITLBEASG 540
    |||
DB 481 YEKDQERRTYTLTKTSTASINNLKPGTYVYFOIRAVTAAGYGNVSPRLDVAITLBEASG 540
QY 541 KMEEATAVSSEQNPVILIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFHS 600
    |||
DB 541 KMEEATAVSSEQNPVILIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFHS 600
QY 601 LYERGDGMKETOHNKKMMIASCRL 626
    |||
DB 601 LYERGDGMKETOHNKKMMIASCRL 626
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RESULT 2

PCT-US96-00419-5
Sequence 5, Application PC/TUS9600419
GENERAL INFORMATION:
APPLICANT: Thomas Cioseck, Axel Ulrich, Birgit
APPLICANT: Millauer
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDKI SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00419
FILING DATE: January 3, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: none
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Marburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 626
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-00419-5

Query Match 100.0%; Score 3338; DB 5; Length 626;
Best Local Similarity 100.0%; Pred. No. 1.3e-298;
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVTQRFPSWIIICYLWLGFAHTGEAQAKEYLLDLSKAQTELEWISSPPSGMEISG 60
    |||
DB 1 MVTQRFPSWIIICYLWLGFAHTGEAQAKEYLLDLSKAQTELEWISSPPSGMEISG 60
QY 61 LDENYPIRTYQVCQVMEPNQNNWLRTNWSKGNARIFVELKFTLRDNCNLSLPGVLTCK 120
    |||
DB 61 LDENYPIRTYQVCQVMEPNQNNWLRTNWSKGNARIFVELKFTLRDNCNLSLPGVLTCK 120
QY 121 EFTNLYYYETDYDTGGRNIRENLVYKIDTIADESFTQDGLGERKMKLNTVEIRIGPLSKK 180
    |||
DB 121 EFTNLYYYETDYDTGGRNIRENLVYKIDTIADESFTQDGLGERKMKLNTVEIRIGPLSKK 180
QY 181 GFYLAFODVACIALVSVKYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
    |||
DB 181 GFYLAFODVACIALVSVKYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPRMCSAAGEWLVPIGKICIKAGYQOKGDTCEPCGRRTYKSSSDLOCSRCPHIS 300
    |||
DB 241 EAENSPPRMCSAAGEWLVPIGKICIKAGYQOKGDTCEPCGRRTYKSSSDLOCSRCPHIS 300
QY 301 FSDREGSSRCECEDGYRRASDPDYVACTRPPSAPQNLIFINQTTVLSLEWSPADNGR 360
    |||
DB 301 FSDREGSSRCECEDGYRRASDPDYVACTRPPSAPQNLIFINQTTVLSLEWSPADNGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQGTGLENDYVTMDLAAHANYTEVEAVNG 420
    |||
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQGTGLENDYVTMDLAAHANYTEVEAVNG 420
QY 421 VSDLSRQRLFAAVSTTTGQAAPSOVSQVWKERYLQRSVOLSQOEPHHPGVITTEYIKY 480
    |||
DB 421 VSDLSRQRLFAAVSTTTGQAAPSOVSQVWKERYLQRSVOLSQOEPHHPGVITTEYIKY 480
QY 481 YEKDQERRTYTLTKTSTASINNLKPGTYVYFOIRAVTAAGYGNVSPRLDVAITLBEASG 540
    |||
DB 481 YEKDQERRTYTLTKTSTASINNLKPGTYVYFOIRAVTAAGYGNVSPRLDVAITLBEASG 540
QY 541 KMEEATAVSSEQNPVILIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFHS 600
    |||
DB 541 KMEEATAVSSEQNPVILIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFHS 600
QY 601 LYERGDGMKETOHNKKMMIASCRL 626
    |||
DB 601 LYERGDGMKETOHNKKMMIASCRL 626
```

RESULT 3

US-08-368-776A-3

Sequence 3, Application US/08368776A

Patent No. 6300482

GENERAL INFORMATION:

APPLICANT: Cioseck, Thomas

APPLICANT: Ullrich, Axel

APPLICANT: Millaue, Birgit

TITLE OF INVENTION: METHODS FOR DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF MDK1

TITLE OF INVENTION: SIGNAL TRANSDUCTION

TITLE OF INVENTION: DISORDERS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/368, 776A

FILING DATE: January 3, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

APPLICATION NUMBER: described below:

APPLICATION NUMBER: none

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 610 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-368-776A-3

Query Match

Best Local Similarity 95.8%; Score 3199; DB 3; Length 610;

Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVOOTRPFSSWIIICITWILGFAHTGEAOAAKEVLLDLSKAQOTLEWISSPPSGWEETISG 60
DB 1 MVOOTRPFSSWIIICITWILGFAHTGEAOAAKEVLLDLSKAQOTLEWISSPPSGWEETISG 60
QY 61 LDENVTPRTYQVOCVMEPNQNNWLRITWISKGNQRIFFELIKFTLRDONSIPGVLGTCK 120
DB 61 LDENVTPRTYQVOCVMEPNQNNWLRITWISKGNQRIFFELIKFTLRDONSIPGVLGTCK 120
QY 121 ETPNLYVETDYGGRNTRRNLYVYKIDITADESTOGDGERKKMLTEVREIGPLSKX 180
DB 121 ETPNLYVETDYGGRNTRRNLYVYKIDITADESTOGDGERKKMLTEVREIGPLSKX 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVPDTVTGSEFSLVEVGTCVSSAEE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVPDTVTGSEFSLVEVGTCVSSAEE 240

DB 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVPDTVTGSEFSLVEVGTCVSSAEE 240
QY 241 EAENSPRMHCSABGEMLVPIGKCI CKAGYQOKGDTCEPCGRPFYKSSSODLQSCRPTHS 300
DB 241 EAENSPRMHCSABGEMLVPIGKCI CKAGYQOKGDTCEPCGRPFYKSSSODLQSCRPTHS 300
QY 301 FSDREGSSRCECEDGYRABSDPPYACTRPPSPAPQNLFININQTVLSLEWSPPADNGR 360
DB 301 FSDREGSSRCECEDGYRABSDPPYACTRPPSPAPQNLFININQTVLSLEWSPPADNGR 360
QY 361 NDVTYRILCKRCSMEQECYPCGSNIGYMPQOGLBNYTVMDLLAHANTFEVAVNG 420
DB 361 NDVTYRILCKRCSMEQECYPCGSNIGYMPQOGLBNYTVMDLLAHANTFEVAVNG 420
QY 421 VSDLSRSQRLFAAVSITTGQAAPSOVSGWKKERYLORSVOLSMQEPHPNGVITEYIKY 480
DB 421 VSDLSRSQRLFAAVSITTGQAAPSOVSGWKKERYLORSVOLSMQEPHPNGVITEYIKY 480
QY 481 YEKDQERTYSTLTCKSTASINNLKPGYVFPQIRAVTAAGYGNYSPLDVATLEBASG 540
DB 481 YEKDQERTYSTLTCKSTASINNLKPGYVFPQIRAVTAAGYGNYSPLDVATLEBASG 540
QY 541 KMFPAIVSSBQNDVYIIIAVAVAGTIIIVPMVFGFIIGRRHCYSKADQGBDELYEHS 600
DB 541 KMFPAIVSSBQNDVYIIIAVAVAGTIIIVPMVFGFIIGRRHCYSKADQGBDELYEHS 600
QY 601 L 601
DB 601 L 601

RESULT 4

PCT-US96-00419-3

Sequence 3, Application PC/TUS9600419

GENERAL INFORMATION:

APPLICANT: Thomas Cioseck, Axel Ullrich, Birgit

APPLICANT: Millaue, Birgit

TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM compatible

OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00419

FILING DATE: January 3, 1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

APPLICATION NUMBER: described below:

APPLICATION NUMBER: none

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 610

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-00419-3

Query Match 95.8%; Score 3199; DB 5; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.8e-286;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTQTRPSPWILLCYIMLGFHAGTGEAQAKEVLLDLSKAQOTLEWISSPPSGWEEISG 60
DB 1 MVTQTRPSPWILLCYIMLGFHAGTGEAQAKEVLLDLSKAQOTLEWISSPPSGWEEISG 60
QY 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGAQRI FVELKFTLRDCLSLPGVLGTCK 120
DB 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGAQRI FVELKFTLRDCLSLPGVLGTCK 120
QY 121 EFTNLYYEEDYDYGKNIENLYVKIDTIADESFTQDGLGERKMLNTEVREIGPLSKK 180
DB 121 EFTNLYYEEDYDYGKNIENLYVKIDTIADESFTQDGLGERKMLNTEVREIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSKVYKWKWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
DB 181 GFYLAFOVDGACIALVSKVYKWKWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPMHCSAEGEWLVPIGKCI CKAQYQOKGDTCEPCGRPFYKSSODLQCSRCPHIS 300
DB 241 EAENSPPMHCSAEGEWLVPIGKCI CKAQYQOKGDTCEPCGRPFYKSSODLQCSRCPHIS 300
QY 301 FSDRESSRCECEGYRRAPSDPPYVACTRPPSPQNLFININQTVTLWSPPADNGGR 360
DB 301 FSDRESSRCECEGYRRAPSDPPYVACTRPPSPQNLFININQTVTLWSPPADNGGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENYVTYMDLAAHYTFEVAVNG 420
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENYVTYMDLAAHYTFEVAVNG 420
QY 421 VSDLSRQRLFAAVSITTTGQAAPSQVSGWKEKRVLQRSVOLSWQEBHPNGVITEYEIKY 480
DB 421 VSDLSRQRLFAAVSITTTGQAAPSQVSGWKEKRVLQRSVOLSWQEBHPNGVITEYEIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVAITLEASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVAITLEASG 540
QY 541 KMEFATVSSSEQNPVILIAVAVAGTIIIVFVWFGFIIGRRHCGYSKADQGBELYFHS 600
DB 541 KMEFATVSSSEQNPVILIAVAVAGTIIIVFVWFGFIIGRRHCGYSKADQGBELYFHS 600
QY 601 L 601
DB 601 L 601

RESULT 5
US-08-368-776A-12
Sequence 12, Application US/08368776A
Patent No. 6300482
GENERAL INFORMATION:
APPLICANT: Ciosek, Thomas
APPLICANT: Ulrich, Axel
APPLICANT: Millauer, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF MDK1
TITLE OF INVENTION: SIGNAL TRANSDUCTION
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California

COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,776A
FILING DATE: January 3, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-368-776A-12

Query Match 95.6%; Score 3191.5; DB 3; Length 994;
Best Local Similarity 95.9%; Pred. No. 8.3e-285;
Matches 605; Conservative 6; Mismatches 15; Indels 5; Gaps 2;

QY 1 MVTQTRPSPWILLCYIMLGFHAGTGEAQAKEVLLDLSKAQOTLEWISSPPSGWEEISG 60
DB 1 MVTQTRPSPWILLCYIMLGFHAGTGEAQAKEVLLDLSKAQOTLEWISSPPSGWEEISG 60
QY 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGAQRI FVELKFTLRDCLSLPGVLGTCK 120
DB 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGAQRI FVELKFTLRDCLSLPGVLGTCK 120
QY 121 EFTNLYYEEDYDYGKNIENLYVKIDTIADESFTQDGLGERKMLNTEVREIGPLSKK 180
DB 121 EFTNLYYEEDYDYGKNIENLYVKIDTIADESFTQDGLGERKMLNTEVREIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSKVYKWKWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
DB 181 GFYLAFOVDGACIALVSKVYKWKWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPMHCSAEGEWLVPIGKCI CKAQYQOKGDTCEPCGRPFYKSSODLQCSRCPHIS 300
DB 241 EAENSPPMHCSAEGEWLVPIGKCI CKAQYQOKGDTCEPCGRPFYKSSODLQCSRCPHIS 300
QY 301 FSDRESSRCECEGYRRAPSDPPYVACTRPPSPQNLFININQTVTLWSPPADNGGR 360
DB 301 FSDRESSRCECEGYRRAPSDPPYVACTRPPSPQNLFININQTVTLWSPPADNGGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENYVTYMDLAAHYTFEVAVNG 420
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENYVTYMDLAAHYTFEVAVNG 420
QY 421 VSDLSRQRLFAAVSITTTGQAAPSQVSGWKEKRVLQRSVOLSWQEBHPNGVITEYEIKY 480
DB 421 VSDLSRQRLFAAVSITTTGQAAPSQVSGWKEKRVLQRSVOLSWQEBHPNGVITEYEIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVAITLEASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVAITLEASG 540

Qy 541 KMFETAVSSQONPVIIIAVAVAGTIIIVMVFQIIIGRRHCGYSKADQSGDEELYFH 600
Db 541 KMFETAVSSQONPVIIIAVAVAGTIIIVMVFQIIIGRRHCGYSKADQSGDEELYFH 600
Qy 601 ----LYRERGOMETQON-KKMIAGSRL 626
Db 601 TKTYIDPETYEDPNRAVHQFAKELDASCIRI 631

RESULT 6

US-08-368-776A-2
; Sequence 2, Application US/08368776A
; Patent No. 6300482
; GENERAL INFORMATION:
; APPLICANT: Ciosek, Thomas
; APPLICANT: Ullrich, Axel
; APPLICANT: Millaer, Birgit
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF MDK1
; TITLE OF INVENTION: SIGNAL TRANSDUCTION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368, 776A
; FILING DATE: January 3, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: none
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-368-776A-2

Query Match 95.6%; Score 3191; DB 3; Length 998;

Best Local Similarity 100.0%; Pred. No. 9.3e-285; Indels 0; Gaps 0;

Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVVOTRPPSWIILCYIMILGFAGTGEAQAQAEVLLDLSKAQOTLEWISSPPSGMEETISG 60
Db 1 MVVOTRPPSWIILCYIMILGFAGTGEAQAQAEVLLDLSKAQOTLEWISSPPSGMEETISG 60
Qy 61 LDENVYTPRTYQVCQVMEPNQNNMLRTNWSKGAQRIFWELKTTLDQNSLPVGLGTCK 120
Db 61 LDENVYTPRTYQVCQVMEPNQNNMLRTNWSKGAQRIFWELKTTLDQNSLPVGLGTCK 120

Db 61 LDENVYTPRTYQVCQVMEPNQNNMLRTNWSKGAQRIFWELKTTLDQNSLPVGLGTCK 120
Qy 121 ETFNLVYETEDYDGRNIRENLVYKIDITIADESFTQDGERKMLNTEVREIGPLSKK 180
Db 121 ETFNLVYETEDYDGRNIRENLVYKIDITIADESFTQDGERKMLNTEVREIGPLSKK 180
Qy 181 GFYLAPODVGACIALVSVKYYKKCWITVENLAVFPDTVTGSEFSSLVEVRGTCVSSAEE 240
Db 181 GFYLAPODVGACIALVSVKYYKKCWITVENLAVFPDTVTGSEFSSLVEVRGTCVSSAEE 240
Qy 241 EAENSPPMHGSAEEMLVPIGKICIKAGYQOKGDTCEPCRRFRFKSSSODIQSCRCTHS 300
Db 241 EAENSPPMHGSAEEMLVPIGKICIKAGYQOKGDTCEPCRRFRFKSSSODIQSCRCTHS 300
Qy 301 FSDREGSSRCECEGGYRAPSDPPYACTPPSPAPQULFININQTTLSLEMSPPADNGR 360
Db 301 FSDREGSSRCECEGGYRAPSDPPYACTPPSPAPQULFININQTTLSLEMSPPADNGR 360
Qy 361 NDVYTRILCKRCSWEGECVPCGSGNIGYMPQQTGLJEDNYVTMDLLAHANTFEVAVNG 420
Db 361 NDVYTRILCKRCSWEGECVPCGSGNIGYMPQQTGLJEDNYVTMDLLAHANTFEVAVNG 420
Qy 421 VSDLSRQRLFAAVSITTGQAAPQVSGWKKERVLQRSVOLSWQEPHPNGVITEYEIKY 480
Db 421 VSDLSRQRLFAAVSITTGQAAPQVSGWKKERVLQRSVOLSWQEPHPNGVITEYEIKY 480
Qy 481 YEKQRERTYSLTKTSKTSASINLKPQYVFOIRAVTAAGYGNYSPPRLDVATLEBASG 540
Db 481 YEKQRERTYSLTKTSKTSASINLKPQYVFOIRAVTAAGYGNYSPPRLDVATLEBASG 540
Qy 541 KMFETAVSSQONPVIIIAVAVAGTIIIVMVFQIIIGRRHCGYSKADQSGDEELYFH 599
Db 541 KMFETAVSSQONPVIIIAVAVAGTIIIVMVFQIIIGRRHCGYSKADQSGDEELYFH 599

RESULT 7

PCT-US96-00419-2
; Sequence 2, Application PC/TUS9600419
; GENERAL INFORMATION:
; APPLICANT: Thomas Ciosek, Axel Ullrich, Birgit
; APPLICANT: Millaer, Birgit
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00419
; FILING DATE: January 3, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: none
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 998
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; PCT: US96-00419-2

Query Match 95.6%; Score 3191; DB 5; Length 998;
 Best Local Similarity 100.0%; Pred. No. 9.3e-285;
 Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVVQTRFSPWIIICYYIMLGFAGTGEAQAKEVLLDLSKAQTELEWISSPPSGMEISG 60
 DB 1 MVVQTRFSPWIIICYYIMLGFAGTGEAQAKEVLLDLSKAQTELEWISSPPSGMEISG 60
 QY 61 LDENYTPIRTYQVCQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDCNSLPGLGTCK 120
 DB 61 LDENYTPIRTYQVCQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDCNSLPGLGTCK 120
 QY 121 ETEFLYYETDVTGGRNIRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGLSKK 180
 DB 121 ETEFLYYETDVTGGRNIRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGLSKK 180
 QY 181 GFYLAQDVAGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAE 240
 DB 181 GFYLAQDVAGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAE 240
 QY 241 EAENSPPMHCSABGEWLVPIGKCI CKAGYQOKGDTCEPCGRFRYKSSODLQCRCPYHS 300
 DB 241 EAENSPPMHCSABGEWLVPIGKCI CKAGYQOKGDTCEPCGRFRYKSSODLQCRCPYHS 300
 QY 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFNINQTVLSLEWSPADNGGR 360
 DB 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFNINQTVLSLEWSPADNGGR 360
 QY 361 NDVTYRILCRKSGMEQECVPCGSNIGYMPQOGLGLEDNYTVMDLHANYTEVEAVNG 420
 DB 361 NDVTYRILCRKSGMEQECVPCGSNIGYMPQOGLGLEDNYTVMDLHANYTEVEAVNG 420
 QY 421 VSDLSRQRLFAAVSITTGQAAPQSVGVKMERVLQSVOLSWQEPHPNVITTEYIKY 480
 DB 421 VSDLSRQRLFAAVSITTGQAAPQSVGVKMERVLQSVOLSWQEPHPNVITTEYIKY 480
 QY 481 YEKQDERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVATLEBASG 540
 DB 481 YEKQDERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVATLEBASG 540
 QY 541 KMFETAVSSBQNVIIIAVAVAGTIIIVMVFGLIIRRHCGYSADQGBELXPH 599
 DB 541 KMFETAVSSBQNVIIIAVAVAGTIIIVMVFGLIIRRHCGYSADQGBELXPH 599

RESULT 8
 US-08-368-776A-11
 ; Sequence 11, Application US/08368776A
 ; Patent No. 6300482

; GENERAL INFORMATION:
 ; APPLICANT: Cioseck, Thomas
 ; APPLICANT: Ullrich, Axel
 ; APPLICANT: Millaue, Birgit
 ; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
 ; TITLE OF INVENTION: AND TREATMENT OF MDK1
 ; TITLE OF INVENTION: SIGNAL TRANSDUCTION
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California

; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: Storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08368, 776A
 ; FILING DATE: January 3, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION DATA: described below: none
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 208/007
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 993 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-368-776A-11

Query Match 94.4%; Score 3151.5; DB 3; Length 993;
 Best Local Similarity 99.2%; Pred. No. 4e-281; Indels 5; Gaps 1;
 Matches 594; Conservative 0; Mismatches 0;

QY 1 MVVQTRFSPWIIICYYIMLGFAGTGEAQAKEVLLDLSKAQTELEWISSPPSGMEISG 60
 DB 1 MVVQTRFSPWIIICYYIMLGFAGTGEAQAKEVLLDLSKAQTELEWISSPPSGMEISG 60
 QY 61 LDENYTPIRTYQVCQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDCNSLPGLGTCK 120
 DB 61 LDENYTPIRTYQVCQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDCNSLPGLGTCK 120
 QY 121 ETEFLYYETDVTGGRNIRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGLSKK 180
 DB 121 ETEFLYYETDVTGGRNIRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGLSKK 180
 QY 181 GFYLAQDVAGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAE 240
 DB 181 GFYLAQDVAGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAE 240
 QY 241 EAENSPPMHCSABGEWLVPIGKCI CKAGYQOKGDTCEPCGRFRYKSSODLQCRCPYHS 300
 DB 241 EAENSPPMHCSABGEWLVPIGKCI CKAGYQOKGDTCEPCGRFRYKSSODLQCRCPYHS 300
 QY 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFNINQTVLSLEWSPADNGGR 360
 DB 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFNINQTVLSLEWSPADNGGR 360
 QY 361 NDVTYRILCRKSGMEQECVPCGSNIGYMPQOGLGLEDNYTVMDLHANYTEVEAVNG 420
 DB 361 NDVTYRILCRKSGMEQECVPCGSNIGYMPQOGLGLEDNYTVMDLHANYTEVEAVNG 420
 QY 421 VSDLSRQRLFAAVSITTGQAAPQSVGVKMERVLQSVOLSWQEPHPNVITTEYIKY 480
 DB 421 VSDLSRQRLFAAVSITTGQAAPQSVGVKMERVLQSVOLSWQEPHPNVITTEYIKY 480
 QY 481 YEKQDERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVATLEBASG 540
 DB 481 YEKQDERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVATLEBASG 540

QY 541 KMFEATAVSSSEONPVIIIAVAVAGTIIIVFVWFPGFIIGRRHCGSKADQEGDEBELYFH 599
DB 540 ----ATAVSSSEONPVIIIAVAVAGTIIIVFVWFPGFIIGRRHCGSKADQEGDEBELYFH 594

RESULT 9
US-08-449-645A-17

; Sequence 17, Application US/08449645A

; Patent No. 5981245

; GENERAL INFORMATION:

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

; TITLE OF INVENTION: Kinases

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Patent Operations/RBW

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,645A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-287

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 998 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-449-645A-17

Query Match

Best Local Similarity 94.0%; Score 3139; DB 2; Length 998;

Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVQTRPSPSWIILCYIWLGFHAGTGEAQAKEVLLDLSKAQOTLEWISSPPSGWEEISG 60
DB 1 MVQTRPSPSWIILCYIWLGFHAGTGEAQAKEVLLDLSKAQOTLEWISSPPSGWEEISG 60
QY 61 LDENTPTIRTYOVQVMEPNQNNMLRTNWSKGNQRIFEVLEKFTLRDQNSLPVLTGCK 120
DB 61 LDENTPTIRTYOVQVMEPNQNNMLRTNWSKGNQRIFEVLEKFTLRDQNSLPVLTGCK 120
QY 121 ETFNLYYETDYDGRNIRENLYVKIDITIADESFQGLDGERKKMLTEVREIIGPLSKK 180
DB 121 ETFNLYYETDYDGRNIRENLYVKIDITIADESFQGLDGERKKMLTEVREIIGPLSKK 180
QY 181 GFYLAFOVAGACIALVSVKYYKKCMTIENLAEPDVTGSEFSSLVEVRGTCVSSAE 240
DB 181 GFYLAFOVAGACIALVSVKYYKKCMTIENLAEPDVTGSEFSSLVEVRGTCVSSAE 240
QY 241 EAENAPRMHCSAEGEWLPVIGKCIKAGYQOKGDTCEPCGRGFYKSSQDLQCSRCPTHS 300
DB 241 EAENAPRMHCSAEGEWLPVIGKCIKAGYQOKGDTCEPCGRGFYKSSQDLQCSRCPTHS 300
QY 301 FSDRSGSSRCCEDEGYRAPSDPPYVACTRPSPAPONLIFNINQTTVSLSENGPPADNGR 360
DB 301 FSDRSGSSRCCEDEGYRAPSDPPYVACTRPSPAPONLIFNINQTTVSLSENGPPADNGR 360
QY 361 NDVTYRIILCKRCMSWEGECVPCGSGNIGVMPQOTGLIEDNYVTVMDLAANVTFFEYAVNG 420
DB 361 NDVTYRIILCKRCMSWEGECVPCGSGNIGVMPQOTGLIEDNYVTVMDLAANVTFFEYAVNG 420

QY 421 VSDLSRQRLFAAVSITTGQAAPSOVSGWMEKRVLQRSVQSWOPEHPNGVITEYIKY 480
DB 421 VSDLSRQRLFAAVSITTGQAAPSOVSGWMEKRVLQRSVQSWOPEHPNGVITEYIKY 480

RESULT 10
US-08-702-367A-17

; Sequence 17, Application US/08702367A

; Patent No. 5981246

; GENERAL INFORMATION:

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

; TITLE OF INVENTION: Kinases

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Patent Operations/RBW

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/702,367A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-287

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 998 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-702-367A-17

Query Match

Best Local Similarity 94.0%; Score 3139; DB 2; Length 998;

Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVQTRPSPSWIILCYIWLGFHAGTGEAQAKEVLLDLSKAQOTLEWISSPPSGWEEISG 60
DB 1 MVQTRPSPSWIILCYIWLGFHAGTGEAQAKEVLLDLSKAQOTLEWISSPPSGWEEISG 60
QY 61 LDENTPTIRTYOVQVMEPNQNNMLRTNWSKGNQRIFEVLEKFTLRDQNSLPVLTGCK 120
DB 61 LDENTPTIRTYOVQVMEPNQNNMLRTNWSKGNQRIFEVLEKFTLRDQNSLPVLTGCK 120
QY 121 ETFNLYYETDYDGRNIRENLYVKIDITIADESFQGLDGERKKMLTEVREIIGPLSKK 180
DB 121 ETFNLYYETDYDGRNIRENLYVKIDITIADESFQGLDGERKKMLTEVREIIGPLSKK 180
QY 181 GFYLAFOVAGACIALVSVKYYKKCMTIENLAEPDVTGSEFSSLVEVRGTCVSSAE 240
DB 181 GFYLAFOVAGACIALVSVKYYKKCMTIENLAEPDVTGSEFSSLVEVRGTCVSSAE 240
QY 241 EAENAPRMHCSAEGEWLPVIGKCIKAGYQOKGDTCEPCGRGFYKSSQDLQCSRCPTHS 300
DB 241 EAENAPRMHCSAEGEWLPVIGKCIKAGYQOKGDTCEPCGRGFYKSSQDLQCSRCPTHS 300

Qy	301	SSDREGSSRCEDDDYRABSPDPYACRPSAPBOMI	FININOTTVLS	ENSPADNGR	360
Db	301	FSDEKSSRCBCEDEGYYRABSPDPYACRPSAPBOMI	FININOTTVLS	ENSPADNGR	360
Qy	361	NDVTRILICKRCSWEGECVPCGSNIGYMPQOTGLE	NDVTVMDLAAHAN	ITTEVEAVNG	420
Db	361	NDVTRILICKRCSWEGECVPCGSNIGYMPQOTGLE	NDVTVMDLAAHAN	ITTEVEAVNG	420
Qy	421	VSDLSRQRLFAAVSITTTGQAPPSQVSGYMKERVL	ORSVOLSMOBEHPN	SVTTEYEIKY	480
Db	421	VSDLSRQRLFAAVSITTTGQAPPSQVSGYMKERVL	ORSVOLSMOBEHPN	SVTTEYEIKY	480
Qy	481	YEKODRERTYSTLKRTKSTASINNLKPGTVYVYFQI	RAVVAAGYGNYS	PRJLVATLEBASG	540
Db	481	YEKODRERTYSTLKRTKSTASINNLKPGTVYVYFQI	RAVVAAGYGNYS	PRJLVATLEBASG	540
Qy	541	KMEFETAVSSSEONPVYITITVVAVAGTITITVPMV	FGTIGRRHCGSKAOD	GGBEELLYFH	599
Db	541	KMEFETAVSSSEONPVYITITVVAVAGTITITVPMV	FGTIGRRHCGSKAOD	GGBEELLYFH	599

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RESULT 11
US-09-949-016-6501
; Sequence 6501, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6501
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6501

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Query Match 94.0%; Score 3139; DB 4 Length 996;
Best Local Similarity 97.7%; Pred. No. 5,8e-280;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0.

QY 1 MVQVTRFPSWIIICYIWMILGFNHTGEAQAANEVLLDSKAQOTELEWISCPSGMEIISG 60
Dd 1 MVQGRYPSWIIICYIWMILFRNHTGEAQAANEVLLDSKAQOTELEWISCPNGMEIISG 60
QY 61 IDENTPPIRTYOVCWMEPNQNNWLRTWISGNAORFVFLKFTLRQCSLIPGLGYCK 120
Dd 61 LDENTPPIRTYOVCWMEPNQNNWLRTWISGNAORFVFLKFTLRQCSLIPGLGYCK 120
QY 121 EFNLYYEETDYDTRNIRENLYVKIDITIADESEFTQDLSGRKKLNTIAREIGPLSKK 180
Dd 121 EFNLYYEETDYDTRNIRENLYVKIDITIADESEFTQDLSGRKKLNTIAREIGPLSKK 180
QY 181 GPYLAFOVQACIALVSKVYKKCWITVENLAVPDVTGSEBSLVEVRGTCVSSABE 240
Dd 181 GPYLAFOVQACIALVSKVYKKCWITVENLAVPDVTGSEBSLVEVRGTCVSSABE 240
QY 241 EAENSPRHCSAGEWMLVPIGKCICKAGQOQGPCECGRRFYSYSSQULQCCSCPHHS 300
Dd 241 EAENSPRHCSAGEWMLVPIGKCICKAGQOQGPCECGRRFYSYSSQULQCCSCPHHS 300
QY 301 FSDRGSSRCECEDGYRAPSDDPYVACTRPPSAFQNTIFINQTTVALIWSPPAANGGR 360
Dd 301 FSDRGSSRCECEDGYRAPSDDPYVACTRPPSAFQNTIFINQTTVALIWSPPAANGGR 360

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D6	301	FSDKESSKRCEDGYRABDPYVACTRPPSAPQNLFININTYVLSMSPADNGR	360
QY	361	NDVTYRILCKRSGMEGECVPCGSGNIYGMPOOTGEDNYVTWDLAHANYTPEVAVNG	420
D6	361	NDVTYRILCKRSGMEGECVPCGSGNIYGMPOOTGEDNYVTWDLAHANYTPEVAVNG	420
QY	421	VSDLSRSQRLPAVAVSTTTGQAAPSOVSGVMKREYVQRSVOLSWQEPHPGVITEYIKY	480
D6	421	VSDLSRSQRLPAVAVSTTTGQAAPSOVSGVMKREYVQRSVOLSWQEPHPGVITEYIKY	480
QY	481	YKDOBERTYSTLKTSISINLKPQTVVYFQIRAVTAAGYNGVSRLLDVATLEBAG	540
D6	481	YKDOBERTYSTLKTSISINLKPQTVVYFQIRAVTAAGYNGVSRLLDVATLEBAG	540
QY	541	KMEEARAVNSQNPVITIAVAVACTITLLPMVGFITIGRPHGCSYKADQGEDELYEH	599
D6	541	KMEEARAVNSQNPVITIAVAVACTITLLPMVGFITIGRPHGCSYKADQGEDELYEH	599

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Query Match	94.0%	Score 3139	DB 5	Length 998
Best Local Similarity	97.7%	Pred. No. 5.8e-280		
Matches	585	Conservative 10	Mismatches 4	Indels 0
				Gaps 0
QY	1	MVVGTRFSPSWIILCYIMLGFPAHTGEAQAQAEVLLDLSKAQOTELEWISSPPSGWEETISG	60	
DB	1	MVFGRRYSWIIILCYIMLRPAHTGEAQAQAEVLLDLSKAQOTELEWISSPPNGWEETISG	60	
QY	61	LDENVTPTRTYQVQCWMEPPNNMLRTNWMISKGAQRIFVFLKLTLPBNCNLLPGVLGTC	120	
DB	61	LDENVTPTRTYQVQCWMEPPNNMLRTNWMISKGAQRIFVFLKLTLPBNCNLLPGVLGTC	120	
QY	121	ETPNLYYYETDYDGTGRNIRENLYKIDTIADESFQGDJGERMKINTVEREIGPLSKK	180	
DB	121	ETPNLYYYETDYDGTGRNIRENLYKIDTIADESFQGDJGERMKINTVEREIGPLSKK	180	
QY	181	GPYLAPODVGACIALVSVKVTYKKCCMTI VENVLAVPDTVTGSEFSSSLVEVFGTCYSSAE	240	
DB	181	GPYLAPODVGACIALVSVKVTYKKCCMTI VENVLAVPDTVTGSEFSSSLVEVFGTCYSSAE	240	

Db 128 NMVFESDDONGRIKENOYIKIDTIADESFTELDIDGRVMTKNTREVDY3PLSKKGFY 187
QY 184 LAFODVACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSAEBEAE 243
Db 188 LAFODVACIALVSVRYKKCPSVRHNLAVFPDITIGADSSQLLEVSQSVN--HSVTD 245
QY 244 NSPRMCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRFRFYKSSODLQCSRCPHSD 303
Db 246 EPPRMCSAEGEWLVPIGKCMCKAGYEKNKGTCCVCRPGFFKASPHIQSCGKCPHSHYTH 305
QY 304 REGSSRCECDGYRRASDPPIVACTRPPSAQNLIENINOTVLSLEMSPPADNGGRNDV 363
Db 306 EEAFTSCVCEKDYFRRESDPPTMACTRPPAPRNALSNVNETSVFLEWLPADTGGKDV 365
QY 364 TYRILCKRCSEWQECVPCGSNIGYMPQOTGLEBDNYTVMDLLAHANYTFEVEAVNGVSD 423
Db 366 SYIACKCKNSHAGVCECGGHVRYLPQSGLNKTSVMWVDLLAHNTYTFEIEAVNGVSD 425
QY 424 LSRSQLFAVSIITGQAAPSOVSQVWKERYLQRSVQLSWQEPHNGVITEYEIKYEEK 483
Db 426 LSPGARQYVSVNVTNOAPSPVTNVKKGKIAKNSISLSWQEPDRPNIGIILEYEIKHFEK 485
QY 484 DQERTYSTLKTSTASINNLKGTYYVFOIRAVTAAGYGNVSPRLDVATLEASGMF 543
Db 486 DQ-ETSTYITIKSKETITTAAGLKPASVYVFOIRARTAGYGVFSRFE-----F 533
QY 544 EAT--AVSSEQNPIIIIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQGDDE-LYFH 599
Db 534 ETTVPFASSDQSQIPVIAVSVTG-VILLAVIGVLLSGRCGYSAKQDPBEKMHFH 592
QY 600 S 600
Db 593 N 593

RESULT 15
US-08-702-367A-13
; Sequence 13, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Amgen Patent Operations/RBM
; STREET: 1840 Denavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702.367A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 991 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-367A-13

Query Match 55.2%; Score 1841; DB 2; Length 991;
Best Local Similarity 57.4%; Pred. No. 2.5e-160;

Matches 345; Conservative 97; Mismatches 133; Indels 26; Gaps 8;
QY 6 RPSW--IILCYIWLGFATGGAQAKEYLILDSKAQOQTELEMISSPESGWEISGLDE 63
Db 13 RAPLMCTLLC-----AALRTILASPSENVNLDSTRTWMDLQIMAFPKMGWEIGVDE 67
QY 64 NYPIRTIYQCVMEPNQNNMLRTNMSKGAORIVELKFTLRDQNSLPGLVGTCKETP 123
Db 68 NYAPIHTYQCKMEQNNMLTWSINSGAGRIFELFTLRDQNSLPGLVGTCKETP 127
QY 124 NLVYERDVTGNTNIRNELLVKIKDITIADESFTQGLDGEKMKLNTREIREIPLSKKGFY 183
Db 128 NMVFESDDONGRIKENOYIKIDTIADESFTELDIDGRVMTKNTREVDY3PLSKKGFY 187
QY 184 LAFODVACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSAEBEAE 243
Db 188 LAFODVACIALVSVRYKKCPSVRHNLAVFPDITIGADSSQLLEVSQSVN--HSVTD 245
QY 244 NSPRMCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRFRFYKSSODLQCSRCPHSD 303
Db 246 EPPRMCSAEGEWLVPIGKCMCKAGYEKNKGTCCVCRPGFFKASPHIQSCGKCPHSHYTH 305
QY 304 REGSSRCECDGYRRASDPPIVACTRPPSAQNLIENINOTVLSLEMSPPADNGGRNDV 363
Db 306 EEAFTSCVCEKDYFRRESDPPTMACTRPPAPRNALSNVNETSVFLEWLPADTGGKDV 365
QY 364 TYRILCKRCSEWQECVPCGSNIGYMPQOTGLEBDNYTVMDLLAHANYTFEVEAVNGVSD 423
Db 366 SYIACKCKNSHAGVCECGGHVRYLPQSGLNKTSVMWVDLLAHNTYTFEIEAVNGVSD 425
QY 424 LSRSQLFAVSIITGQAAPSOVSQVWKERYLQRSVQLSWQEPHNGVITEYEIKYEEK 483
Db 426 LSPGARQYVSVNVTNOAPSPVTNVKKGKIAKNSISLSWQEPDRPNIGIILEYEIKHFEK 485
QY 484 DQERTYSTLKTSTASINNLKGTYYVFOIRAVTAAGYGNVSPRLDVATLEASGMF 543
Db 486 DQ-ETSTYITIKSKETITTAAGLKPASVYVFOIRARTAGYGVFSRFE-----F 533
QY 544 EAT--AVSSEQNPIIIIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQGDDE-LYFH 599
Db 534 ETTVPFASSDQSQIPVIAVSVTG-VILLAVIGVLLSGRCGYSAKQDPBEKMHFH 592
QY 600 S 600
Db 593 N 593

Search completed: August 23, 2005, 08:27:36
Job time : 23.7783 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 71.9191 Seconds
(without alignments) 3366.450 Million cell updates/sec

Title: US-10-073-064-5
Perfect score: 3338
Sequence: 1 MVVQTRPPSMILICYWLG.....DGMEKTOHKKMKIASCSRL 626

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	# Query Match	Length	DB ID	Description
1	3338	100.0	626	2	AAW03423 Mouse dev
2	3199	95.8	610	2	AAW03422 Mouse dev
3	3191	95.6	998	2	AAW03421 Mouse dev
4	3139	94.0	945	8	ADM87167 Human pro
5	3139	94.0	998	2	AAW03421 Mouse dev
6	1841	55.2	991	2	AAW03421 Mouse dev
7	1830.5	54.8	953	5	ABP52826 Human rec
8	1822	54.6	1005	2	AAW03421 Mouse dev
9	1817	54.4	1037	5	ABG61868 Prostate
10	1817	54.4	1037	5	ABG61868 Prostate
11	1806.5	54.1	975	5	ABP52827 Human Etk
12	1796	53.8	983	3	AAW03421 Mouse dev
13	1796	53.8	983	3	AAW03421 Mouse dev
14	1796	53.8	983	3	AAW03421 Mouse dev
15	1796	53.8	983	3	AAW03421 Mouse dev
16	1796	53.8	983	3	AAW03421 Mouse dev
17	1796	53.8	983	3	AAW03421 Mouse dev
18	1796	53.8	983	3	AAW03421 Mouse dev
19	1796	53.8	983	3	AAW03421 Mouse dev
20	1787.5	53.6	984	7	ADD48947 Human Pro
21	1787.5	53.6	984	7	ADD48947 Human Pro
22	1775.5	53.2	983	2	AAW03421 Mouse dev
23	1770	53.0	983	2	AAW03421 Mouse dev
24	1741.5	52.2	833	7	ADM29344 Human nov
25	1741.5	52.2	921	5	ABG79685 Tumour in

26	1741.5	52.2	949	7	ADM29342 Human nov
27	1741.5	52.2	986	2	AAW03421 Mouse dev
28	1741.5	52.2	986	2	AAW03421 Mouse dev
29	1741.5	52.2	986	8	ADQ17780 Human sof
30	1741.5	52.2	986	8	ADP54599 Human Etk
31	1741.5	52.2	997	4	ABG05689 Novel hum
32	1741.5	52.2	1026	4	ABG22931 Novel hum
33	1737.5	52.1	539	3	AAW03421 Mouse dev
34	1734.5	52.0	986	2	AAW03421 Mouse dev
35	1701.5	51.0	935	8	ADP43499 Human Etk
36	1701.5	51.0	935	8	ADP43499 Human Etk
37	1701.5	51.0	992	4	AAW03421 Mouse dev
38	1701.5	51.0	992	5	ABP69349 Human pol
39	1701.5	51.0	1005	8	ADP43499 Human Etk
40	1701.5	51.0	1005	8	ADP43499 Human Etk
41	1701.5	51.0	1005	8	ADP43499 Human Etk
42	1701.5	51.0	1012	4	AAW03421 Mouse dev
43	1699.5	50.9	935	8	ADP43499 Human Etk
44	1699.5	50.9	935	8	ADP43499 Human Etk
45	1671	50.1	1035	5	ABG70391 Human Etk

ALIGNMENTS

RESULT 1	AAW03423	standard; protein; 626 AA.
ID	AAW03423	
XX	AAW03423	
AC	AAW03423	
DT	11-NOV-1996	(first entry)
XX		
DE	Mouse developmental kinase 1 MDK1 T2.	
XX		
KW	Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase; RTK; signal transduction; probe; diagnosis; gene therapy; neurodegeneration; neuroproliferation; cancer.	
KW		
XX		
OS	Mus sp.	
XX		
FX	Key	Location/Qualifiers
FT	Peptide	1..28
FT		/label= sig_peptide
FT	Modified-site	64..66
FT		/label= N-glycosylation_site
FT	Modified-site	343..345
FT		/label= N-glycosylation_site
FT	Modified-site	410..412
FT		/label= N-glycosylation_site
FT	Domain	555..579
FT		/label= Transmembrane domain
FT	Misc-difference	600..626
FT		/note= "product of alternative splicing"
XX		
XX	W09621013-A1.	
PD	11-JUL-1996.	
XX		
PF	03-JAN-1996;	96W0-US000419.
XX		
PR	03-JAN-1995.	95US-00368776.
XX		
PA	(SUGEN-) SUGEN INC.	
PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.	
PI	Closesek T, Ullrich A, Millaer B;	
XX		
DR	WPI: 1996-333988/33.	
DR	N-PSDB; AAT32962.	
XX		
PT	New mouse development kinase 1 gene - used for developing prods. for diagnosis and treatment of abnormalities in signal transduction pathways.	

XX Example 1; Page 113-115; 128pp; English.
PS CDNA cloning using adult mouse brains and Northern blotting identified 2
XX truncated versions, Mdk1 T1 (AAW03422) and Mdk1 T2 (AAW03423), of the
CC novel mouse developmental kinase 1 (MDK1) (see also AAW03421), a new
CC member of the eck/eph family of receptor tyrosine kinases. Their amino
CC acid sequences were deduced from cDNA clones (AA132961 and AA132962)
CC obtd. from adult mouse brains. Mdk T1 and T2 each possess the entire
CC ectodomain, the transmembrane domain and part of the juxtamembrane region
CC of Mdk1, but lack the catalytic tyrosine kinase domain. They can be used
CC to screen for potential agents useful for treatment of diseases
CC characterised by abnormal signal transduction
XX

Sequence 626 AA;

Query Match 100.0%; Score 3338; DB 2; Length 625;
Best Local Similarity 100.0%; Pred. No. 1e-286; Indels 0; Gaps 0;
Matches 626; Conservative 0; Mismatches 0;

QY 1 MVTQTFPSWIIICYLWLGFAHTGSAQAKEYLLDLSKAQOTELEWISSPSGWEISG 60
DB 1 MVTQTFPSWIIICYLWLGFAHTGSAQAKEYLLDLSKAQOTELEWISSPSGWEISG 60
QY 61 LDENYPIRITYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLRDQNSLPVGLGTCK 120
DB 61 LDENYPIRITYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLRDQNSLPVGLGTCK 120
QY 121 EFTNLYYYETDYDTGIRNIRENLVYKIDITLADSFQDGLGERKMKLNTVEVEIGPLSKK 180
DB 121 EFTNLYYYETDYDTGIRNIRENLVYKIDITLADSFQDGLGERKMKLNTVEVEIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVVEVGTCVSSAE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVVEVGTCVSSAE 240
QY 241 EAENSPPMHCSAGSEWLVPIGKCI CKAGYOQKGDTPCGRRRYKSSSDLOCRCPTHS 300
DB 241 EAENSPPMHCSAGSEWLVPIGKCI CKAGYOQKGDTPCGRRRYKSSSDLOCRCPTHS 300
QY 301 FSPREGSSRCECEGYYRAPSDPPYVACTRPPSAPOQLININQTTVLSLMSPPADNGR 360
DB 301 FSPREGSSRCECEGYYRAPSDPPYVACTRPPSAPOQLININQTTVLSLMSPPADNGR 360
QY 361 NDVTYRILCKRCGMEQECVPCGSNIGYMPQOTGLEBNYTVNDLAHANYTEVEAVNG 420
DB 361 NDVTYRILCKRCGMEQECVPCGSNIGYMPQOTGLEBNYTVNDLAHANYTEVEAVNG 420
QY 421 VSDLSRSQRLFAVSVITTGQAAPSQVSGWKERYLQRSVLSQEPHPHNVITTEYIKY 480
DB 421 VSDLSRSQRLFAVSVITTGQAAPSQVSGWKERYLQRSVLSQEPHPHNVITTEYIKY 480
QY 481 YEEDQRERTYSTLTKTSSTASINNLKPGTYVFOIRVTAAGYGNVSPRLDVTLEBASG 540
DB 481 YEEDQRERTYSTLTKTSSTASINNLKPGTYVFOIRVTAAGYGNVSPRLDVTLEBASG 540
QY 541 KMEEATAVSSEONPVIIIAVAVAGTIIIVFWVFGFLIGRRHCGYSKADGDBELYFHS 600
DB 541 KMEEATAVSSEONPVIIIAVAVAGTIIIVFWVFGFLIGRRHCGYSKADGDBELYFHS 600
QY 601 LYREBGGMGKTKQHNKKMTASCSRL 626
DB 601 LYREBGGMGKTKQHNKKMTASCSRL 626

RESULT 2
ID AAW03422 standard; protein; 610 AA.

XX AAW03422;
XX AAW03422;
DT 11-NOV-1996 (first entry)
XX

DE Mouse developmental kinase 1 Mdk1 T1.
XX Mouse developmental kinase 1; Mdk1 T1; receptor tyrosine kinase; RTK;
XX signal transduction; probe; diagnosis; gene therapy; neurodegeneration;
KM neuroproliferation; cancer.
XX
OS Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..28 /label= Sig_peptide
FT Modified-site 64..66 /label= N-glycosylation_site
FT Modified-site 343..345 /label= N-glycosylation_site
FT Modified-site 410..412 /label= N-glycosylation_site
FT Domain 555..579 /label= Transmembrane_domain
FT Misc-difference 600..610 /note= "Product of alternative splicing"
FT
FT
PN MO9621013-A1.

XX 11-JUL-1996.
XX 03-JAN-1996; 96WO-US000419.
XX 03-JAN-1995; 95US-00368776.
XX (SUGR-) SUGEN INC.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX Closek T, Ullrich A, Millaer B;
PI WPI, 1996-333988/33.
XX N-PSDB; AA132961.
DR New mouse development kinase 1 gene - used for developing prods. for
XX diagnosis and treatment of abnormalities in signal transduction pathways.
PT
PS Example 1; Page 109-111; 128pp; English.
XX
XX CDNA cloning using adult mouse brains and Northern blotting identified 2
CC truncated versions, Mdk1 T1 (AAW03422) and Mdk1 T2 (AAW03423), of the
CC novel mouse developmental kinase 1 (MDK1) (see also AAW03421), a new
CC member of the eck/eph family of receptor tyrosine kinases. Their amino
CC acid sequences were deduced from cDNA clones (AA132961 and AA132962)
CC obtd. from adult mouse brains. Mdk T1 and T2 each possess the entire
CC ectodomain, the transmembrane domain and part of the juxtamembrane region
CC of Mdk1, but lack the catalytic tyrosine kinase domain. They can be used
CC to screen for potential agents useful for treatment of diseases
CC characterised by abnormal signal transduction
XX
XX Sequence 610 AA;
Query Match 95.8%; Score 3199; DB 2; Length 610;
Best Local Similarity 100.0%; Pred. No. 2.6e-276; Indels 0; Gaps 0;
Matches 601; Conservative 0; Mismatches 0;

Db	181	GFYLAFOVGNACIALVSVKVVYKKCKMTIYENLAVFPDVTGSGFSFLVBRGTCVSSAE	240
Qy	241	EAENSPRMHCSAEGEWLVPIGKCI CKAGYQOKGDTCEPCGRAPFYKSSODLOCSRCP	THS 3000
Db	241	EAENSPRMHCSAEGEWLVPIGKCI CKAGYQOKGDTCEPCGRAPFYKSSODLOCSRCP	THS 3000
Qy	301	FSDRGSGSRCEDEGYRAPSPDPPIYACTRPPSAPONLIFININOTVLSLEMSPPADNGR	3600
Db	301	FSDRGSGSRCEDEGYRAPSPDPPIYACTRPPSAPONLIFININOTVLSLEMSPPADNGR	3600
Qy	361	NDVTRILICRKCSEWGECVPCGSNTGMPQOQTGLEDNTVTWMDLAAHANYTEVEAVNG	420
Db	361	NDVTRILICRKCSEWGECVPCGSNTGMPQOQTGLEDNTVTWMDLAAHANYTEVEAVNG	420
Qy	421	VSDLSRSORLFAAVSITTTGOAAPSOVSGVMKEKRVLORSVOLSMQEBEHPNGVITTEI	480
Db	421	VSDLSRSORLFAAVSITTTGOAAPSOVSGVMKEKRVLORSVOLSMQEBEHPNGVITTEI	480
Qy	481	YEKQDREBRTYSTLTKTSTKSASINNLKPGTVVYVQIARVATYAGYNTSPRLDVATLE	540
Db	481	YEKQDREBRTYSTLTKTSTKSASINNLKPGTVVYVQIARVATYAGYNTSPRLDVATLE	540
Qy	541	KMFEEATVASSSEONPVYIIIAVAVAGTIIIVFWFGIIGRRHCGYSKADOGGEELYFHS	6000
Db	541	KMFEEATVASSSEONPVYIIIAVAVAGTIIIVFWFGIIGRRHCGYSKADOGGEELYFHS	6000
Qy	601	L 601	
Db	601	L 601	

XX	RESULT 3
XX	AAW034421
XX	ID AAW034421 standard; protein; 998 AA.
XX	AC AAW034421;
XX	DT 11-NOV-1996 (first entry)
XX	DE Mouse developmental kinase 1.
XX	KW Mouse developmental kinase 1; MDK1; receptor tyrosine kinase; RTK;
XX	KW signal transduction; probe; diagnosis; therapy; neurodegeneration;
XX	KM neuroproliferation; cancer.
XX	OS Mus sp.
XX	XX
FH	Key
FT	Location/Qualifiers
FT	Peptide
FT	1..28
FT	/label= Sig_peptide
FT	Modified-site
FT	64..66
FT	/label= N-glycosylation_site
FT	Modified-site
FT	343..345
FT	/label= N-glycosylation_site
FT	Modified-site
FT	410..412
FT	/label= N-glycosylation_site
FT	Domain
FT	555..579
FT	/label= Transmembrane_domain
XX	XX
XX	PN WO9621013-A1.
XX	XX
XX	DD 11-JUL-1996.
XX	XX
XX	PF 03-JAN-1996; 96WO-US000419.
XX	XX
XX	PR 03-JAN-1995; 95US-00368776.
XX	XX
PA	(SUGC-) SUGEN INC.
PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX	XX
PI	Cloosek T, Ullrich A, Millauer B;
XX	XX

DR	WPI: 1996-333988/33.
DR	N-PSDB: AAT32960.
XX	
PT	New mouse development kinase 1 gene - used for developing prods. for
XX	diagnosis and treatment of abnormalities in signal transduction pathways.
XX	
PS	Example 1; Page 105-108; 128pp; English.
XX	
CC	Mouse development kinase 1 (MDK1) (AAW03421) is a new member of the
CC	ecf/epb family of receptor tyrosine kinases (RTKs). Its amino acid
CC	sequence was deduced from a cDNA clone (AAT32960) isolated from mouse
CC	embryo and adult brain libraries. The distinct patterns of MDK1
CC	expression during mouse development suggest an important role for MDK1 in
CC	the formation of neuronal structures. MDK1 may be obt'd. by expression in
CC	host cells. It can be used in methods for the diagnosis of disease
CC	characterised by abnormality in a signal transduction pathway, such as
CC	neuroproliferative or neurodegenerative disorders or cancer, to screen
CC	for (ant)agonists, and to raise antibodies
SQ	Sequence 998 AA;

Query Match	Score	DB 2	Length
95.6%	3191	DB 2	998
Best Local Similarity	100.0%	Pred. No. 3e-275	
Matches	599	Conservative	0
		Mismatches	0
		Indels	0
		Gaps	0

QY	DB	Sequence	Score	DB 2	Length
QY	1	MMVOTRPPSWIILCYIWLGFATHGGAQAQKEVLLDLSKAQOOTELEWISSPPSGMEIRISG	60		
DB	1	MMVOTRPPSWIILCYIWLGFATHGGAQAQKEVLLDLSKAQOOTELEWISSPPSGMEIRISG	60		
QY	61	LDENYTPIRTYQVCQVMEPNQNNLRTNWSISKNAQRI FVELKFTLDDCNSLPGLGCTCK	120		
DB	61	LDENYTPIRTYQVCQVMEPNQNNLRTNWSISKNAQRI FVELKFTLDDCNSLPGLGCTCK	120		
QY	121	ETFMLYYYEYDYPDGRNIRENLYKIDTTIADESFPTGDLGERGKAKNTEVREIGPLSKK	180		
DB	121	ETFMLYYYEYDYPDGRNIRENLYKIDTTIADESFPTGDLGERGKAKNTEVREIGPLSKK	180		
QY	181	GFYLAPODVGCIALVSKVKKKCMWIIIVENLAFPTLVGSEFSSLVYVRGTCVSSABE	240		
DB	181	GFYLAPODVGCIALVSKVKKKCMWIIIVENLAFPTLVGSEFSSLVYVRGTCVSSABE	240		
QY	241	EAENSPPMHCSAEGEMLVPIGKICICAKAYOOKGDTCEPCGRFPYKSSSODLQSCRCPHS	300		
DB	241	EAENSPPMHCSAEGEMLVPIGKICICAKAYOOKGDTCEPCGRFPYKSSSODLQSCRCPHS	300		
QY	301	FSDEGSSRCECEDGYRAPSDPEPYVACTRPPSAPNLI FNINQTTVLSLEWSPADNGR	360		
DB	301	FSDEGSSRCECEDGYRAPSDPEPYVACTRPPSAPNLI FNINQTTVLSLEWSPADNGR	360		
QY	361	NDVTYRILCKRCWEGCEVPCGSGNIGYMPQGTGLENNYTTWMDLHANYTEFEVAVNG	420		
DB	361	NDVTYRILCKRCWEGCEVPCGSGNIGYMPQGTGLENNYTTWMDLHANYTEFEVAVNG	420		
QY	421	VSDLSRQRLFAANISITTTGQAAPQVSGWKKERLQDSVQLSMQEPHPNCVITREYAIKY	480		
DB	421	VSDLSRQRLFAANISITTTGQAAPQVSGWKKERLQDSVQLSMQEPHPNCVITREYAIKY	480		
QY	481	YEKQRRERTSTLTKTSGSINNLKRGTYVYFDIRAVTAAGYGNYSPRLDVATLEBASG	540		
DB	481	YEKQRRERTSTLTKTSGSINNLKRGTYVYFDIRAVTAAGYGNYSPRLDVATLEBASG	540		
QY	541	KMFETAVSSBONFVILIAVAVAGTIIILVMFGFIIIGRRHCYSGRADQGBELFYH	599		
DB	541	KMFETAVSSBONFVILIAVAVAGTIIILVMFGFIIIGRRHCYSGRADQGBELFYH	599		

RESULT 4	ID	AD	XX	XX
ADM87167	ADM87167	standard; protein; 945 AA.		
ADM87167;				
03-JUN-2004 (first entry)				

XX Human protein SEQ ID NO:260.
 DE
 XX
 XX
 KM respiratory; cytoskeletal; antiarthritic; antiinflammatory;
 KM gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
 KM antineuritic; gene therapy; molecular weight marker; chromosome marker;
 KM chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
 KM inflammatory condition; arthritis; inflammatory bowel disease;
 KM Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
 KM graft versus host disease; human.
 XX
 OS Homo sapiens.
 PN WO2004009834-A2.
 XX
 PD 29-JAN-2004.
 XX
 PF 19-JUL-2002; 2002MO-US022858.
 XX
 PR 21-JUL-2001; 2001US-0306971P.
 PR 28-MAR-2002; 2002US-00112944.
 XX
 PA (NUVE-) NUVELO INC.
 XX
 PI Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
 PI Weinman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
 PI WPI; 2004-143291/14.
 DR N-PSDB; ADM66923.
 XX
 PT New isolated polynucleotides and polypeptides, useful for treating, e.g.
 PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
 PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
 PT versus host disease.
 XX
 PS Claim 20; SEQ ID NO 260; 591pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I): (a)
 CC comprising a nucleotide sequence selected from SEQ ID NO:1-344; or (b)
 CC which encodes a polypeptide with biological activity, where the
 CC polynucleotide hybridises to (I) under stringent hybridisation conditions
 CC or has greater than 99% sequence identity with (I). (I) has respiratory,
 CC cytoskeletal, antiarthritic, antiinflammatory, gastrointestinal,
 CC antibacterial, immunosuppressive, antidiabetic and antineuritic
 CC activities, and can be used in gene therapy. (I) can be used for
 CC generating polynucleotides encoding chimeric or fusion proteins and
 CC heterologous protein sequences. The polynucleotides can be used to
 CC express recombinant protein for analysis, characterisation or therapeutic
 CC use; as markers for tissues in which the corresponding protein is
 CC preferentially expressed; as molecular weight markers on gels; as
 CC chromosome markers or tags to identify chromosomes or to map related gene
 CC positions; to compare with endogenous DNA sequences in patients to
 CC identify potential genetic disorders; as probes to hybridise and discover
 CC genes, related DNA sequences; as a source of information to derive PCR
 CC primers for genetic fingerprinting; as a probe to substract-out known
 CC sequences in the process of discovering other novel polynucleotides; for
 CC selecting and making oligomers for attachment to a gene chip or other
 CC support, including for examination of expression patterns; to raise anti-
 CC protein antibodies using DNA immunisation techniques; and as an antigen
 CC to raise anti-DNA antibodies or elicit another immune response. The
 CC polynucleotides and polypeptides can also be used as nutritional sources
 CC or supplements, e.g. as a protein or amino acid supplement, as a carbon
 CC source, as a nitrogen source or as a source of carbohydrates. The
 CC polynucleotides and polypeptides can also be used treat cancer. The
 CC compositions are useful for promoting better or faster closure of non-
 CC healing wounds, for the generation and regeneration of tissues, for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, and conditions resulting from
 CC systemic cytokine damage. The compositions can also be used to treat
 CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
 CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
 CC or graft versus host disease. The present sequence represents a novel
 CC human polypeptide sequence from the present invention. N.B. The sequences

CC for this patent were obtained from the USPTO web site from an equivalent
 CC US patent US20040048249A1.
 CC
 XX
 XX
 CC Sequence 945 AA;
 SQ
 Query Match 94.0%; Score 3139; DB 8; Length 945;
 Best Local Similarity 97.7%; Pred. No. 1,2e-270;
 Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MVTQTFPFWIITCYTWLGFPAHTGEAQAKEYLLDLSAQOETELEMISPPGMEISG 60
 DB 1 MVTQTFPFWIITCYTWLGFPAHTGEAQAKEYLLDLSAQOETELEMISPPGMEISG 60
 QY 1DENYTPIRTYQYQVMEPNQNNMTNMI SKNAQRIVELEKFTLRDCNSLPGVLTCK 120
 DB 1DENYTPIRTYQYQVMEPNQNNMTNMI SKNAQRIVELEKFTLRDCNSLPGVLTCK 120
 QY 121 EFTNLYYYETDPTDGTGNIRENLVYKIDTIAADESFTQGLGERKMLNTEVRIGPLSK 180
 DB 121 EFTNLYYYETDPTDGTGNIRENLVYKIDTIAADESFTQGLGERKMLNTEVRIGPLSK 180
 QY 181 GFYLAFOYGAACIALSVKYYKKCWTIVENLAVPDTYGSFSSLVEVRGTCVSSAEE 240
 DB 181 GFYLAFOYGAACIALSVKYYKKCWTIVENLAVPDTYGSFSSLVEVRGTCVSSAEE 240
 QY 241 EAENSFRMHCASAGEWLVPIGKICIKAGYQOKGDTCEPCGRPFYKSSSODLQCSRPTHS 300
 DB 241 EAENSFRMHCASAGEWLVPIGKICIKAGYQOKGDTCEPCGRPFYKSSSODLQCSRPTHS 300
 QY 301 FSDRESSSRCECDGYYRAPSDPPYACRPPAPQNLFINQTTVSLSEWSPADNGR 360
 DB 301 FSDRESSSRCECDGYYRAPSDPPYACRPPAPQNLFINQTTVSLSEWSPADNGR 360
 QY 361 NDVTYRIILCKRCSEWGECPGCSNIGYMPQGTGLDNTVYWDLLAHNYTFEVAVNG 420
 DB 361 NDVTYRIILCKRCSEWGECPGCSNIGYMPQGTGLDNTVYWDLLAHNYTFEVAVNG 420
 QY 421 VSDLSRSQRLFAVSIITGQAAPSOVGVKKEVILQRSVQLSQWEPHEHNGVITEYIKY 480
 DB 421 VSDLSRSQRLFAVSIITGQAAPSOVGVKKEVILQRSVQLSQWEPHEHNGVITEYIKY 480
 QY 481 YENDQGERYSTLTKTSTASTNNLKPQVYVYQIRAVYAAAGVNSPPLDVATLLEAAG 540
 DB 481 YENDQGERYSTLTKTSTASTNNLKPQVYVYQIRAVYAAAGVNSPPLDVATLLEAAG 540
 QY 541 KMFETAVSSEQNPIIIVAVAGTIIIVFWFGIIRRHGYSKADQEGDELYFH 599
 DB 541 KMFETAVSSEQNPIIIVAVAGTIIIVFWFGIIRRHGYSKADQEGDELYFH 599
 RESULT 5
 AAR85092
 ID AAR85092 strand; protein; 998 AA.
 XX
 AC AAR85092;
 XX
 DT 16-APR-1996 (first entry)
 XX
 DE EPH-like receptor protein tyrosine kinase HEK11.
 XX
 KW EPH-like receptor protein tyrosine kinase; PK; HEK11;
 KW human eph-like kinase; therapy; diagnosis; antibody; vector.
 OS Homo sapiens.
 XX
 PN WO9528484-A1.
 XX
 PD 26-OCT-1995.
 XX
 PF 14-APR-1995; 95WO-US004681.
 XX
 PR 15-APR-1994; 94US-00229509.
 XX

PA (AMGE-) AMGEN INC.
 XX Fox GM, Welcher AA, Jing S;
 XX WPI; 1995-373799/48.
 DR N-PSDB; AAT02949.
 XX
 PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and
 PT related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation or
 PT prodn.
 XX
 PS Claim 18; Page 71-75; 133pp; English.
 CC
 CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain
 CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11
 CC shows no homology to any known EPH-like receptor. Recombinant HEK
 CC receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host cells,
 CC and are used to produce antibodies (utilised in diagnostic assays), or to
 CC identify and purify ligands for HEK receptors, or therapeutically to
 CC modulate the activation of cell-associated receptors
 CC
 XX Sequence 998 AA:
 SQ
 Query Match 94.0%; Score 3139; DB 2; Length 998;
 Best Local Similarity 97.7%; Pred. No. 1.3e-270;
 Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MVNTRFSSWIIICWILGFAHNGEAAKEVILLDSKAQOTLEWISSPPSGWEIISG 60
 DB 1 WVFQTRPSWIIICWILGFAHNGEAAKEVILLDSKAQOTLEWISSPPSGWEIISG 60
 QY 1 LDEVTPIRTYOVQVMEPNQNNMLRTNMISKGNORIFVELKFTLRDQNSLPVLTGTCK 120
 DB 61 LDEVTPIRTYOVQVMEPNQNNMLRTNMISKGNORIFVELKFTLRDQNSLPVLTGTCK 120
 QY 121 ETPNLYYETDYGGRNIRENLYVKIDITIADESFTQDGLGERKMKLNTVEIREIGPLSKK 180
 DB 121 ETPNLYYETDYGGRNIRENLYVKIDITIADESFTQDGLGERKMKLNTVEIREIGPLSKK 180
 QY 181 GFYLAFOVGACIALVSKYVYKKCWITVENLAVPDTVTGSEBSLVEVGTCTVSSABE 240
 DB 181 GFYLAFOVGACIALVSKYVYKKCWITVENLAVPDTVTGSEBSLVEVGTCTVSSABE 240
 QY 241 EAENSPRMHGSAEGEMLVPIGKICIKAGYQOKGDTCECGRRFYKSSSQDLCSCRPTHS 300
 DB 241 EAENSPRMHGSAEGEMLVPIGKICIKAGYQOKGDTCECGRRFYKSSSQDLCSCRPTHS 300
 QY 301 FSDREGSSRCCEBDGYRAPSDPPYVACTRPPSAPQNLIFINQTTVSLSEWSPPADNGR 360
 DB 301 FSDREGSSRCCEBDGYRAPSDPPYVACTRPPSAPQNLIFINQTTVSLSEWSPPADNGR 360
 QY 361 NDVYTRILCKKCSWEGSCVPCGSGNIGYMPQOTGLEDDYVYVMDLAAANTFFEEAANG 420
 DB 361 NDVYTRILCKKCSWEGSCVPCGSGNIGYMPQOTGLEDDYVYVMDLAAANTFFEEAANG 420
 QY 421 VSDLSRSORFLAAVSIITGGAAPSOVSGVMEKERVQSRVLSQMOPEHPNGVITFEIKY 480
 DB 421 VSDLSRSORFLAAVSIITGGAAPSOVSGVMEKERVQSRVLSQMOPEHPNGVITFEIKY 480
 QY 481 YEKQREKRTYSTLKTKSTASINMLKPGTVYVFOIRAYTAAGYGNYSRDLVATLEASG 540
 DB 481 YEKQREKRTYSTLKTKSTASINMLKPGTVYVFOIRAYTAAGYGNYSRDLVATLEASG 540
 QY 541 KMFEATAVSSRONPVIITIAVAVAGTITLVFVNEFFIIGRRHCGSKADQGBDELYPH 599
 DB 541 KMFEATAVSSRONPVIITIAVAVAGTITLVFVNEFFIIGRRHCGSKADQGBDELYPH 599

RESULT 6
 AAR85090
 ID AAR85090 standard; protein; 991 AA.
 XX
 AC AAR85090;
 XX
 DT 16-APR-1996 (first entry)
 XX
 DE EPH-like receptor protein tyrosine kinase HEK7.
 XX
 KM EPH-like receptor protein tyrosine kinase; PT; HEK7.
 KM human eph-like kinase; therapy; diagnosis; vector; antibody.
 XX
 OS Homo sapiens.
 XX
 PN W09528484-A1.
 XX
 PD 26-OCT-1995.
 XX
 PF 14-APR-1995; 95WO-US004681.
 XX
 PR 15-APR-1994; 94US-00229509.
 XX
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Welcher AA, Jing S;
 DR WPI; 1995-373799/48.
 DR N-PSDB; AAT02947.
 XX
 PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and
 PT related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation or
 PT prodn.
 XX
 PS Claim 18; Page 54-57; 133pp; English.
 CC
 CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain
 CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11
 CC shows no homology to any known EPH-like receptor. Recombinant HEK
 CC receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host cells,
 CC and are used to produce antibodies (utilised in diagnostic assays), or to
 CC identify and purify ligands for HEK receptors, or therapeutically to
 CC modulate the activation of cell-associated receptors. Soluble HEK7
 CC receptor may primarily affect cell proliferation and/or differentiation of
 CC brain cells. pancreatic cells
 CC
 XX Sequence 991 AA:
 SQ
 Query Match 55.2%; Score 1841; DB 2; Length 991;
 Best Local Similarity 57.4%; Pred. No. 1.4e-154;
 Matches 345; Conservative 97; Mismatches 133; Indels 26; Gaps 8;
 QY 6 RFPSSW--IILCYTWLGFHNGEAAKEVILLDSKAQOTLEWISSPPSGWEIISGIDE 63
 DB 13 RAPLMTCILLC-----AALRTLLASPSNEVILLDSRTVMGLGVIAPPKMMEBIGEVDE 67
 QY 64 NYTPIRTYOVQVMEPNQNNMLRTNMISKGNORIFVELKFTLRDQNSLPVLTGTCKETF 123
 DB 64 NYTPIRTYOVQVMEPNQNNMLRTNMISKGNORIFVELKFTLRDQNSLPVLTGTCKETF 127
 QY 124 NLVYETDYGGRNIRENLYVKIDITIADESFTQDGLGERKMKLNTVEIREIGPLSKKGFY 183
 DB 128 NMYVFSDDQNGRNIRKNOYIKIDITIADESFTLDDGRVMKLNTEVREIVDVGPLSKKGFY 187
 QY 184 LAFODVGACIALVSKYVYKKCWITVENLAVPDTVTGSEBSLVEVGTCTVSSABEAB 243
 DB 188 LAFODVGACIALVSKYVYKKCPVVRHLAVFPDITIGADSSQLLEVSGSCVN--HSVTD 245

```

QY 244 NSPRMCSAAGEWLVPIGKCI CKAGYQOKDPTCEPCGRFRFYKSSODLQCSRCPTHSFD 303
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 246 EPPMHCSAAGEWLVPIGKCMCKAGYEKNGTCCVCPPEFFKASPHIQSGCKCPHSYTH 305
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 304 REGSSRECEDDGYRAPSDPYVACTPAPAPQLININQTYSLFMSPADNGENDV 363
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 306 EBSSTSCVCEKDFRRESDEPTMACTPSPAPRAISNVETSVEFLWITPADTGKRDV 365
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 364 TYRILCRKCSWEGECVPCSGNIGYMPQOTGLENDYTVMDLAAHANYTEVEAVANGVD 423
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 366 SYTIACKCKNSHAGVCECGHVRYLRLRQGLKNTSVMWDLAHTNYTEIEKAVNVSD 425
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 424 LSSSQRLFAAVSITTGGAAPSQVSGVKKERYLQSRVLSQEPHEHNGVITETIKYRK 483
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 426 LSPGARQVSVNVTYNQAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILLEYEIKHFEK 485
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 484 DOBERTYSTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVLTLEBASGMF 543
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 486 DQ-ETSTITIKSKETTITAGLKPASVYVFOIRAKTAGVFSRRPE-----F 533
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 544 EAT---AVSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGSKADCEGDEE-LYFH 539
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 534 ETTTPVFPAASDQSQIPVIAVSIVG-VILLAVIGVLSSGRRCGYSKAKCDPEEKMHFH 592
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 600 S 600
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 593 N 593
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 7

ABP52826

ID ABP52826 standard; protein; 953 AA.

XX ABP52826;

DT 31-OCT-2002 (first entry)

XX Human receptor protein-tyrosine kinase SEQ ID NO:7.

XX Human; kinase; enzyme; inflammation; cancer; psoriasis; gene therapy;

XX arteriosclerosis; antiinflammatory; cytostatic; antipsoriatic;

XX antiarteriosclerotic.

XX Homo sapiens.

XX MO200257432-A2.

XX 25-JUL-2002.

XX 02-JAN-2002; 2002MCO-US000112.

XX 02-JAN-2001; 2001US-00751389.

XX (PEKE) PE CORP.

XX Guegler K, Webster M, Di Francesco V, Beasley EM;

XX WPI; 2002-599718/64.

XX New peptides encoded by genes within the human genome useful for treating

XX disorders associated with abnormal expression of kinase, e.g.

XX inflammation, cancer, arteriosclerosis, in drug screening assays and

XX pharmacogenomic analysis.

XX Disclosure; Fig 2G-H; 346pp; English.

XX The present invention describes a human kinase protein (I), located on

XX chromosome 3. (I) has antiinflammatory, cytosolic, antipsoriatic and

XX antiarteriosclerotic activities, and can be used in gene therapy. (I)

XX peptides can be used in substantial and specific assays related to

XX functional information of the peptide sequences, to raise antibodies or

XX to elicit immune response, as reagents in assays to determine the levels

XX of protein in biological fluids, and as markers for tissues where the

CC corresponding protein is expressed. The peptides and antibodies are
 CC useful in drug screening assays, tissue typing and pharmacogenomic
 CC analysis. They are also useful in treating disorders associated with the
 CC absence of, inappropriate, or unwanted expression of the kinase protein,
 CC e.g. inflammation, cancer, arteriosclerosis, and psoriasis. The nucleic
 CC acid molecules encoding (I) can be used for probes, primers and chemical
 CC intermediates in biological assays, for constructing recombinant vectors,
 CC expressing antigenic portions of the protein. The peptide and nucleic
 CC acid sequences are useful as models for the development of human
 CC therapeutic targets, aid in the identification of therapeutic proteins
 CC and serve as targets for the development of human therapeutic agents that
 CC modulate kinase activity in cells and tissues that express the kinase.
 CC The present sequence represents a protein given in comparison with the
 CC human kinase protein of the present invention

SQ Sequence 953 AA;

Query Match 54.8%; Score 1830.5; DB 5; Length 953;

Best Local Similarity 58.8%; Pred. No. 1.1e-153;

Matches 338; Conservative 95; Mismatches 123; Indels 19; Gaps 6;

```

QY 30 AKSVLLDSKAQQTLEWITSSPPSGWBEISGLBENTPTRTYOVCOVMEPNQNMILRTNW 89
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 SNEVNLDSRTTNGDLGWIAPFKGMBEIGEVENAPLHTTVQCVKMEQNQNMILLTSW 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 90 ISKNAQRIFVELKFTLRDQNSLPGLVIGTCKETFNLYYYETDYDGRNIRENLVYKIDTI 149
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ISNEGASRIPIELKFTLRDQNSLPGLVIGTCKETFNLYYYETDYDGRNIRENLVYKIDTI 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 150 ADESTFGDGLGRKKAKLNTVAEIEIPLSKGYLAFOVDGACIALVSKVYRYKKCMTIV 209
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ADESEFTELDIDRVKMLNTEVADVGPLSKKGYLAFOVDGACIALVSVRYRYKKCPSSV 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 210 ENLAVFPDVTGSEFSLVEVRGTQVSSAEAEENSPRMHCSAAGEWLVPIGKICAGY 269
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 RHLAVFPDITITGADSSQDLVESSCVN--HSYDDEPKMHCSEGEWLVPIGKICAGY 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 270 QOKGDTCEPCGRFRFYKSSODLQCSRCPTHSFSDREGSSRCECEDGYRAPSDPYVACT 329
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 239 EEKNGTCQVCRPGFPKASPHIQSGCKCPHSYTHEASISVCCEKDFRRESDPPTMAC 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 330 RPSAPQNLIFNINQTYSLFMSPPADNGRNDVYTRILCRCSWEGECVPCSGSNIGYM 389
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 299 RPSAPRMAISNNETSVELEWITPADTGKRDVSVYIACKKNSHAGVCECGHVRYL 358
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 390 POOTGLENDYTVMDLAAHANYTFEVEAVANGVSDLSRSQRLFAAVSITTGGAAPSQVSGV 449
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 359 PROSGLKNTSVMWDLAHTNYTFEIEAVNGVSDLSPGARQVSVNVTYNQAPSPVTNV 418
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 450 MKERVLRQSVOLSQEPHEHNGVITYEIKYKEDQREERTYTLTKTSTASINNLKPGT 509
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 419 KKGIKANSISLSWQEPDRPNGIILLEYEIKHFEKQD-ETSYTIKSKETTITTAGLKPAS 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 510 VYVFOIRATAAGYGVSPRLDVATLEBASGKMFET---AVSSEONPVIIIAVAVAGT 566
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 VYVFOIRARTAAAGYGVFSRRPE-----FETTPVFPAASDQSQIPVIAVSIVG- 525
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 567 IIVFMVFGFIIGRRHCGSKADQEGDEE-LYFHS 600
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 526 VILLAVIGVLSSGRRCGYSKAKQDPEEKMHFH 560
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 8

AAM83147

ID AAM83147 standard; protein; 1005 AA.

XX AAM83147;

XX 11-FEB-1999 (first entry)

XX Rat receptor tyrosine kinase Etk-1.

XX Receptor tyrosine kinase; Ror-1; Ror-2; Etk-1; Etk-2; detection;

XX

XX

XX

KM neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
 KM binding protein; BDNF; NT-3; diagnosis.
 XX Rattus sp.
 OS US5843749-A.
 XX PN
 XX 01-DEC-1998.
 PD
 XX 06-JUN-1995; 95US-00469537.
 PF
 XX 26-JUL-1991; 91US-00736559.
 PR 28-OCT-1993; 93US-00144992.
 PR 17-MAR-1995; 95US-00406247.
 XX
 PA (REG-) REGENERON PHARM INC.
 XX
 PI Maslakowski P, Yancopoulos GD, Maisompierre PC;
 XX WPI: 1999-044584/04.
 DR N-PSDB; AAV70207.
 XX
 PT DNA encoding receptor tyrosine kinase proteins - and corresponding
 PT proteins.
 XX
 PS Example; Fig 22; 194pp; English.
 XX
 CC The present invention describes nucleic acid molecules for Ror-1, Ror-2,
 CC euk-1 and euk-2. Also described are the corresponding proteins: Ror-1,
 CC Ror-2; Euk-1, and Euk-2. The proteins are orphan receptor tyrosine
 CC kinases. The present sequence represents rat Euk-1
 CC
 SQ Sequence 1005 AA;
 Query Match 54.6%; Score 1822; DB 2; Length 1005;
 Best Local Similarity 55.2%; Pred. No. 7.1e-153;
 Matches 349; Conservative 95; Mismatches 136; Indels 52; Gaps 10;
 QY 6 RFPSEWILCY-----IM-----LLGFHNGEQAQAKVLLDSKAQOTLEWISSPPSG 54
 DB 25 RVPASLAGCYSAPIKGPMLTCLCALRTLLASPSNEVNLDSRTVLGDLGWIAPKNG 84
 QY 55 WEBSIGLDENYTPRTYOVQVMEPNONNMLRTWISKGNQRI FVELKFTLRDQNSLPG 114
 DB 85 WEBSIGLDENYAPRHTYOVCKVMEONONNMLTSMISGSRIFILKFTLRDQNSLPG 144
 QY 115 VLGTCKETPNLYETDYDTGRNIRENLYKIDITIADESTQDGLGRKKNLTVREI 174
 DB 145 GLGTCKETPNMYEPESDDENGRNKENQYIKIDITIADESTFELDLGDRVMKLNTEVRDV 204
 QY 175 GPLSKGFYLAFOVGACIALVSVKYYKKWTIVENLAVPDPVTGSEFSLVENVGTC 234
 DB 205 GPLSKGFYLAFOVGACIALVSVKYYKKCPVVRHLAVPDPVTGADSSQLLEVSGSC 264
 QY 235 VSSAEBAENSPRMAAGSEGLVPIGKICAKYQKQGDCEFCGRFRYSSSODLQCS 294
 DB 265 VN--HSTYDDPRKMHGAEGLMVLPIGKCKAKAEEENGCCYCRPFRFASHSQTCS 322
 QY 295 RCPHSPSDBRGSSRCCEGDGYRAPSDDPYVACTRPPSAPQNLIPINOTTVSLWSP 354
 DB 323 KCPHSTHHEASTSCVCEKDYFRRESPPPTMACTRPPSAPRANISVNETSVLEWMP 382
 QY 355 ADNGRNDYTRILICRCKSMWQEGCVPGSGNIGMPOGTGLJEDYVYVMDLAAANTFE 414
 DB 383 ADTGKGADVSYILLCKKCNHAGVCEGCGHVRLLPQIGLKNYSVMADPLAHTNTPFE 442
 QY 415 VEAVNGVDSLRSORLFAAVSITGQAAPSOVSGVMKERVQSRVQSLWQEPHPNGVIT 474
 DB 443 IEAVNGVDSLSPGRQYVSVVTTNQAAPSPVTNVKKGKIKAKNISLSWQEPDPNGIIL 502
 QY 475 EYEIKYEEKQREFTYTLTKYSTASINNLKPGTVVYFQIRAVTAAGYNGYSPRLDVA 534
 DB 503 EYEIKYEEKQD-ETSYTIKSKETTLTAEGIKPASYVVFQIRARTAGYGVFSRRFE-- 558

QY 535 LBEASGMFEATAY---SSQNPIIYAVAVAGTILVEMVRFII-----GRR- 581
 DB 559 -----FETTPFGASNDQSQPIIGSVTVGVILAVMI-GFLSGSCCEGCGRAS 609
 QY 582 -----HCGYSKADQEGDEE-LYFHS 600
 DB 610 SLCAVAHPSLIWRCGYSKAKQDPEEKQMFHN 641
 RESULT 9
 ABR44241
 ID ABR44241 standard; protein; 1037 AA.
 XX
 AC ABR44241;
 XX
 XX 18-AUG-2003 (first entry)
 DT
 DE Tyrosine kinase EHK-1.
 XX
 KM CD81; neuron; neural degeneration; astrocyte; Nrs1; cytosolic; EHK-1;
 KM neuroprotective; nootropic; antiparkinsonian; anticonvulsant; human;
 KM cerebroprotective; gene therapy; tyrosine kinase.
 OS
 OS Homo sapiens.
 XX
 PN WO2003040333-A2.
 XX
 XX 15-MAY-2003.
 PD
 PF 07-NOV-2002; 2002MO-US035588.
 XX
 PR 07-NOV-2001; 2001US-0344712P.
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
 PI Weinstein DE, Suarez C, Zerlin M;
 XX
 DR WPI: 2003-441557/41.
 DR N-PSDB; ACC78163.
 XX
 PT Enhancing survival of neurons, useful for treating neural degeneration
 PT (e.g. Alzheimer's disease) or a defect in astrocyte proliferation (e.g.
 PT astrocytosis), comprises contacting the neurons with CD81 protein or its
 PT derivative.
 XX
 PS Claim 29; Fig 28; 59pp; English.
 PS
 CC The invention relates to enhancing survival of neurons and involves
 CC contacting the neurons with CD81 protein or CD81 derivative, or its
 CC stabilized variants, in an amount that enhances survival of the neurons.
 CC The method is useful for treating neural degeneration or a condition
 CC associated with a defect in astrocyte proliferation in a mammal, and
 CC involves activating Nrs1 or CD81 in the mammal. The method is useful in
 CC treating neural degeneration (e.g. Alzheimer's disease, amyotrophic
 CC lateral sclerosis, Binswanger's disease, Huntington's chorea, multiple
 CC sclerosis, myasthenia gravis, Parkinson's disease, Pick's disease,
 CC cerebral palsy, congenital hydrocephalus, muscular dystrophy, stroke or
 CC vascular dementia) or a condition associated with a defect in astrocyte
 CC proliferation, such as astrocytosis or astrocytoma. The present sequence
 CC represents a the EHK-1 protein (the Nrs1 protein has been previously
 CC identified as an orphan receptor tyrosine kinase termed EHK-1 -GenBank
 CC Accession No. XM_046083.2.)
 CC
 XX
 SQ Sequence 1037 AA;
 Query Match 54.6%; Score 1822; DB 6; Length 1037;
 Best Local Similarity 55.7%; Pred. No. 7.4e-153;
 Matches 347; Conservative 96; Mismatches 132; Indels 48; Gaps 10;
 QY 6 RFPSEW--IILCYWLLGFHNGEQAQAKVLLDSKAQOTLEWISSPPSGWEISGLDE 63
 DB 37 RAPLMTCLILC-----AALRTLLASPSNEVNLDSRTVMGDLGWIAPKNGWEISGRVDE 91

QY 64 NYPIRTYQVQVMEPNQNNMLRTNWSKGNARI FVELKFTLRDNCNSLPGLGTCKETP 123
 DB 92 NYAPIHTYQVCKMEQNNWMLTWSINEGASRI FLEKFTLRDNCNSLPGLGTCKETP 151
 QY 124 NLYYEFDYDTGNIRINENLYKIDTIADESFTQDGERKMKLNTVEBREL3PSKKGfy 183
 DB 152 NMYYFESDDQNGRIKENOYIKIDTIADESFTELDIDGRVMMKNTVEBREL3PSKKGfy 211
 QY 184 LAFQDVACIALVSVKYYKKCMWTIENLAVFPDPTVGSSEPSLVEVRGTCVSAABEAE 243
 DB 212 LAFQDVACIALVSVKYYKKCMWTIENLAVFPDPTVGSSEPSLVEVRGTCVSAABEAE -HSVTD 269
 QY 244 NSPRMCSAEGEWLVPIGKICCKAGYQOKDPTCEPCGRFRFYKSSODLQCSRCPTSPSD 303
 DB 270 EPPRMCSAEGEWLVPIGKICCKAGYBEKNGTCQVCRPFEPFKASPHIQSCGKCPHSHYTH 329
 QY 304 REGSSRECEDEGYRRASDPDYVACTPPSAPQNLININQTTVLSWSPFADNGRNDV 363
 DB 330 EEASTSCVCEKDYFRRESDEPTWACTPPSAPRNAISNVETSVLEWIPFADTGGRKDV 389
 QY 364 TYRILCRGSEWEGECVPCGSNIGYMPQOTGLEDNVYTMDLAHANYTFEEVEAVNGVSD 423
 DB 390 SYTIACKCKNSHAGVCECGHRYLPRQGLKNTSVMMDLANTYTFEEVEAVNGVSD 449
 QY 424 LSRNSQLFAAVSITTGQAAPSOVSGVWKERVLQRSVLSQOEPEHNGVITTEYIKYK 483
 DB 450 LSPGARQYVSVMVTTNQAAPSPVTNVKKGKIAKNSISLSQOEPDRPNGIILEYEIKYFEK 509
 QY 484 DQERTYSTLKTSTASINNLKGTYYVFOIRAVTAAGYNSPRLDVANILEASGKMF 543
 DB 510 DQ-ETSYTIKSKETITTAGLKPASVYFOIRARTAGYGVFSRPE-----F 557
 QY 544 EAT---AVSSEQNPVLIIVAVAGTIIIVFVVGFI-----GRR----- 581
 DB 558 ETPVPFAASDDQOIPVIAVSVTWG-VILLAVIGVLSSGCEGCGRAKSLCAVAHPS 616
 QY 582 ---HGYSKADQEGDEE-LYFHS 600
 DB 617 LWRGCGYKAKQDPEEEMHFNH 639
 RESULT 10
 ABG61868
 ID ABG61868 standard; protein; 1037 AA.
 AC ABG61868;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE Prostate cancer-associated protein #69.
 XX
 OS Prostate cancer; prostate tumour tissue; human; mammal; cycostatic.
 XX
 PN Mammalia.
 PD WO200230268-A2.
 PD 18-APR-2002.
 PF 12-OCT-2001; 2001MO-US032045.
 PR 13-OCT-2000; 2000US-00687576.
 PR 08-DEC-2000; 2000US-00733288.
 PR 08-DEC-2000; 2000US-00733742.
 PR 24-JAN-2001; 2001US-0263957P.
 PR 16-MAR-2001; 2001US-0276791P.
 PR 16-MAR-2001; 2001US-0276888P.
 PR 06-APR-2001; 2001US-0281922P.
 PR 24-APR-2001; 2001US-0286214P.
 PR 30-APR-2001; 2001US-00847046.
 PR 04-MAY-2001; 2001US-0286589P.
 XX

PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 XX WPI: 2002-471335/50.
 DR N-PSDB; ABK92183.
 DR
 PT Detecting a prostate cancer-associated transcript in a cell in a patient,
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
 PT by determining if prostate cancer-associated genes are expressed in a
 PT prostate tissue.
 XX
 PS Claim 27, Page 354; 436pp; English.
 XX
 XX The present invention relates to methods of detecting a prostate cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with prostate cancer-
 CC associated polynucleotides (designated PC genes) that selectively
 CC hybridize to a sequence that is at least 80% identical to them. The
 CC prostate cancer-associated polynucleotide sequences are differentially
 CC expressed in prostate tumour tissue or in prostate cancer and are derived
 CC from the tissues of various organisms such as humans or other mammals
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
 CC associated genes are useful for diagnosing or treating prostate cancer,
 CC as well as for identifying modulators of prostate cancer or agents that
 CC inhibit prostate cancer. The nucleic acid sequences are particularly
 CC useful in gene therapy, as a vaccine or in antisense applications.
 CC ABG61800-ABG61944 represent prostate cancer-associated proteins
 XX
 SQ Sequence 1037 AA;
 Query Match 54.4%; Score 1817; DB 5; Length 1037;
 Best Local Similarity 55.5%; Pred. No. 2,1e-152;
 Matches 346; Conservative 97; Mismatches 132; Indels 48; Gaps 10;
 QY 6 RFPSS--IILCYTWLGFPAHTGEAQAKEYVLDSQAQOLETEWISSPSPGWEIEIGLDE 63
 DB 37 RAPLWMLCLLC-----AAURLTLASPSNEVNLDSRTVWGDLQWIAFPKNGWEIEIYDE 91
 QY 64 NYPIRTYQVQVMEPNQNNMLRTNWSKGNARI FVELKFTLRDNCNSLPGLGTCKETP 123
 DB 92 NYAPIHTYQVCKMEQNNWMLTWSINEGASRI FLEKFTLRDNCNSLPGLGTCKETP 151
 QY 124 NLYYEFDYDTGNIRINENLYKIDTIADESFTQDGERKMKLNTVEBREL3PSKKGfy 183
 DB 152 NMYYFESDDQNGRIKENOYIKIDTIADESFTELDIDGRVMMKNTVEBREL3PSKKGfy 211
 QY 184 LAFQDVACIALVSVKYYKKCMWTIENLAVFPDPTVGSSEPSLVEVRGTCVSAABEAE 243
 DB 212 LAFQDVACIALVSVKYYKKCMWTIENLAVFPDPTVGSSEPSLVEVRGTCVSAABEAE -HSVTD 269
 QY 244 NSPRMCSAEGEWLVPIGKICCKAGYQOKDPTCEPCGRFRFYKSSODLQCSRCPTSPSD 303
 DB 270 EPPRMCSAEGEWLVPIGKICCKAGYBEKNGTCQVCRPFEPFKASPHIQSCGKCPHSHYTH 329
 QY 304 REGSSRECEDEGYRRASDPDYVACTPPSAPQNLININQTTVLSWSPFADNGRNDV 363
 DB 330 EEASTSCVCEKDYFRRESDEPTWACTPPSAPRNAISNVETSVLEWIPFADTGGRKDV 389
 QY 364 TYRILCRGSEWEGECVPCGSNIGYMPQOTGLEDNVYTMDLAHANYTFEEVEAVNGVSD 423
 DB 390 SYTIACKCKNSHAGVCECGHRYLPRQGLKNTSVMMDLANTYTFEEVEAVNGVSD 449
 QY 424 LSRNSQLFAAVSITTGQAAPSOVSGVWKERVLQRSVLSQOEPEHNGVITTEYIKYK 483
 DB 450 LSPGARQYVSVMVTTNQAAPSPVTNVKKGKIAKNSISLSQOEPDRPNGIILEYEIKYFEK 509
 QY 484 DQERTYSTLKTSTASINNLKGTYYVFOIRAVTAAGYNSPRLDVANILEASGKMF 543
 DB 510 DQ-ETSYTIKSKETITTAGLKPASVYFOIRARTAGYGVFSRPE-----F 557
 QY 544 EAT---AVSSEQNPVLIIVAVAGTIIIVFVVGFI-----GRR----- 581

Db 558 ETTVPFAASSDQSGIPVIAVSIVG-VILLAVIGVLLSGSCRCGGRASSLCAVAHPI 616
Qy 582 ---HCGYSKADQEGDEE-LYFHS 600
Db 617 LIWRGYSKAKQDPEEKMHFN 639

RESULT 11
ADE31683
ID ADE31683 standard; protein; 1037 AA.
XX
XX ADE31683;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human 1419 protein #SEQ ID 40.
XX
XX Antiartherosclerotic; cardiact; vasotropic; antiinflammatory;
XX thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
XX cardiovascular disorder; ischaemia; aortic bending;
XX vascular heart disease; endocarditis; atrial fibrillation; heart failure;
XX angina; cardiomyopathy; cardiac death.
XX
XX Homo sapiens.
XX
XX WO2003065984-A2.
XX
XX 14-AUG-2003.
XX
XX 29-JAN-2003; 2003WO-US002571.
XX
XX 01-FEB-2002; 2002US-0353224P.
XX 15-MAR-2002; 2002US-0354529P.
XX 19-APR-2002; 2002US-0373861P.
XX 29-APR-2002; 2002US-0376287P.
XX 12-JUN-2002; 2002US-0388080P.
XX 24-JUN-2002; 2002US-0390971P.
XX 03-JUL-2002; 2002US-0394130P.
XX 10-JUL-2002; 2002US-0394797P.
XX 21-AUG-2002; 2002US-0404904P.
XX 23-AUG-2002; 2002US-0405450P.
XX 04-SEP-2002; 2002US-0408070P.
XX 06-NOV-2002; 2002US-0424300P.
XX 05-DEC-2002; 2002US-0431042P.
XX 05-DEC-2002; 2002US-0431079P.
XX
XX (MILL-) MILENNIUM PHARM INC.
XX
XX Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghy M,
PI Stragliano N, Perodin J, Rodrigue-Way A,
XX
XX WPI; 2003-731468/69.
XX
XX N-PSDB; ADE31682.
XX
XX
XX Identifying a compound capable of treating a cardiovascular disorder
PT (e.g. atherosclerosis) comprises assaying the ability of the compound to
PT modulate the expression or activity of e.g. 1682, 6169 or 6193
PT polypeptide or nucleic acid.
XX
XX
XX Disclosure; SEQ ID NO 40; 328bp; English.
XX
XX The invention relates to a method for identifying a compound capable of
XX treating a cardiovascular disorder. The present invention identifies the
XX differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
XX 43726, 69292, 21656, 32427, 2402, 7747, 1720, 60491, 1371, 7077,
XX 33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 3394, 3484,
XX 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
XX 2868, 283, 2854, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,
XX 19489, 21833, 2317, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1432 or
XX 6585 genes in cardiovascular disease states. The methods are useful in
XX diagnosing, preventing and treating cardiovascular disorders, such as
XX atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,

CC restenosis, arterial inflammation, vascular wall remodeling, coronary
CC microembolism, tachycardia, bradycardia, pressure overload, aortic
CC bending, coronary artery ligation, vascular heart disease, valvular
CC disease, including but not limited to, valvular degeneration caused by
CC calcification, rheumatic heart disease, endocarditis, or complications of
CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
CC heart failure, sinus node dysfunction, angina, heart failure,
CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
CC including but not limited to, pericardial effusion and pericarditis;
CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
CC artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
CC cardiovascular developmental disorders. The methods may also be used for
CC identifying compounds that modulate cardiovascular disorders. Sequences
CC given in ADE31644-ADE31769 represent the genes and proteins that may be
CC regulated by a compound of the invention.
XX
XX
XX Sequence 1037 AA;
XX
XX
XX Query Match 54.4%; Score 1817; DB 7; Length 1037;
XX Best Local Similarity 55.5%; Pred. No. 2.1e-152;
XX Matches 346; Conservative 97; Mismatches 132; Indels 48; Gaps 10;
Qy 6 RFPSSW--IIICYYIWLGFHTGEOAAKEVLLDSKAQOTELEWISSPPSGWBERISGIDE 63
Db 37 RAPIMTCLLLC-----AALRTLLASPSNEVNLDSRTVMGDIGIAPKNGMEIGEVDE 91
Qy 64 NYTPFIRTYOVCQWEPNQNWLRTNWSKGNARIFVELKFTLRDCLSLPGVLTCKETP 123
Db 92 NYAPIHITYOVCKWEOQNWNMLTSMISNEGASRIFTELKFTLRDCLSLPGVLTCKETP 151
Qy 124 NLVYFETDVTGGRNIRNLYVKIDITIADESFTGDDGERKMKLNTVREIGPLSKGFY 183
Db 152 NMYTFESDDQNGRNKIKNOYIKIDITIADESFTLGDGRVMTNTVRYDVGPSKGFY 211
Qy 184 LAFQDVACIALVSVKYYKCKWTIVENLAVFPDVTGSEFSSILVEVGTGVSSAEBAE 243
Db 212 LAFQDVACIALVSVRYKKCPVNHVLAFFPTITIGADSSQLLEVSQCVN--HSVTD 269
Qy 244 NSPMMHCSAGEMLVPIGKICIKAGYQKQDTCPCRRRYKSSQLQSCRCTHPSFD 303
Db 270 EPPMHCASAGEMLVPIGKICIKAGYQKQDTCPCRRRYKSSQLQSCRCTHPSFD 329
Qy 304 REGSSRCEGDEGYRAPSDDPYVACRPPAPQNLIFINQTTVSLMSPADNGGRNDV 363
Db 330 BEASTSCVCEKDFRRESDDPTMACTRPAPRAIASNVNETSVELEWIPADTGCKDV 389
Qy 364 TYRILCRCSMEQGEVPCGSNIGYMPQOTGLEDDNYTVMDLAAHANYFEVAVNGVSD 423
Db 390 SYTIACKCKNSHAGVCEGCGHRYLPKROGLKNTSMMVMDLAHNTYFEIEAVNGVSD 449
Qy 424 LSRSQRLPAVSTTGOAPSOVSGVKEKERYLQSRVOLSQOEBPHNGVITTEIKYK 483
Db 450 LSPGARQYVSVNTQAAAPSVTVKPKRIAKNSISLSQOEBPHNGVITTEIKYK 509
Qy 484 DQRENTSTLKTSTKSTASINNLKRGTYVFOIRAVTAAGVNSPRDVATLEBASGMF 543
Db 510 DQ-STSTYTIKSKETTTAGLKPASVYVFOIRARTAGVGVFSRPE-----F 557
Qy 544 EAT---AVSSEONPVIIVAAVAGTIIIVFWFGFTI-----GRR----- 581
Db 558 ETTVPFAASSDQSGIPVIAVSIVG-VILLAVIGVLLSGSCRCGGRASSLCAVAHPI 616
Qy 582 ---HCGYSKADQEGDEE-LYFHS 600
Db 617 LIWRGYSKAKQDPEEKMHFN 639

RESULT 12
ABP52827 standard; protein; 975 AA.
XX
XX ID ABP52827
XX
XX ABP52827;
AC

XX 31-OCT-2002 (first entry)
XX Human Eph-1 receptor tyrosine kinase protein SEQ ID NO:8.
XX
XX
XX Human; kinase; enzyme; inflammation; cancer; psoriasis; gene therapy;
XX arteriosclerosis; antiinflammatory; cytostatic; antipsoriatic;
XX antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX W0200257432-A2.
XX
XX 25-JUL-2002.
XX
XX 02-JAN-2002; 2002KO-US000112.
XX
XX 02-JAN-2001; 2001US-00751389.
XX
XX (PEKE) PE CORP.
XX
XX Guegler K, Webster M, Di Francesco V, Beasley EM;
XX WPI; 2002-559718/64.
XX
XX New peptides encoded by genes within the human genome useful for treating
XX disorders associated with abnormal expression of kinase, e.g.,
XX inflammation, cancer, arteriosclerosis, in drug screening assays and
XX pharmacogenomic analysis.
XX
XX Disclousure; Fig 2H-J; 346pp; English.
XX
XX The present invention describes a human kinase protein (I), located on
XX chromosome 3. (I) has antiinflammatory, cytostratic, antipsoriatic and
XX antiarteriosclerotic activities, and can be used in gene therapy. (I)
XX peptides can be used in substantial and specific assays related to
XX functional information of the peptide sequences, to raise antibodies or
XX to elicit immune response, as reagents in assays to determine the levels
XX of protein in biological fluids, and as markers for tissues where the
XX corresponding protein is expressed. The peptides and antibodies are
XX useful in drug screening assays, tissue typing and pharmacogenomic
XX analysis. They are also useful in treating disorders associated with the
XX absence of, inappropriate, or unwanted expression of the kinase protein,
XX e.g. inflammation, cancer, arteriosclerosis, and psoriasis. The nucleic
XX acid molecules encoding (I) can be used for probes, primers and chemical
XX intermediates in biological assays, for constructing recombinant vectors,
XX expressing antigenic portions of the protein. The peptide and nucleic
XX acid sequences are useful as models for the development of human
XX therapeutic targets, aid in the identification of therapeutic proteins
XX and serve as targets for the development of human therapeutic agents that
XX modulate kinase activity in cells and tissues that express the kinase.
XX The present sequence represents a protein given in comparison with the
XX human kinase protein of the present invention
XX
XX Sequence 975 AA:
SQ
Query Match 54.1%; Score 1806.5; DB 5; Length 975;
Best Local Similarity 56.8%; Pred. No. 1.6e-151;
Matches 339; Conservative 95; Mismatches 122; Indels 41; Gaps 8;
QY 30 AKEVLLDSRAQOQTELEWISSPSGMEISGLDENYPTIFTYOVCOWEPNONNMRLRTNW 89
DB 1 SNEVNLDSRTWGDGLGIMAFPKKGMEIEGVDENYPIHTYQVCKMEQNONNMRLTSW 60
QY 90 ISKGNORIEVELKFTLRDONSILPGVLGCKETPNLYVYTDVDTGNTRENIYVKIDTI 149
DB 61 ISNBGASRIETLEKFTLRDONSILPGGLGCKETPNMYTFSDONGNINIKENDYIKIDTI 120
QY 150 AADESFTQDGLGRKMKLANTVEEIGPLSKKGFYLAFOVDGACIALYVAVYKKCWTV 209
DB 121 AADESFTQDGLGRKMKLANTVEEIGPLSKKGFYLAFOVDGACIALYVAVYKKCWTV 180
QY 210 ENLAVPDTVTGSEFSSLVEVRGTCVSSAEDEANSPRMHCSABGEWLVEIGKICCKAGY 269

DB 181 RHIAVFPDITITGADSSQLLEVGSGCVN--HSYUDEBPKNHCSABGEWLVEIGKCKAGY 238
QY 270 OOKGDTCEPCGGRFFYSSSQDLQCSRCPTHSFSDRGSSRCEDGYRAPSPYVACT 329
DB 239 EEKNGTCQVCRPFPAASHIOSCGKCPHSTTHEBASISCYCEKDYFRRESDPIMACT 298
QY 330 RPPSAPONTLFINQTTVSLSEWSPPADNGRNDVYRLLCKRCSWEGECVPCGSNIGYM 389
DB 299 RPPSAPRMAISNVNETSVFLEWIPPADTGKRDVSYIACKKCNHAGVCEECGHVRYL 358
QY 390 PQQTGLEEDNYVYMDLAAANTTFEYEAANGVSDLSRQRLPAVSIITGQAAPQVSGY 449
DB 359 PQSGLKNTSVMMVDLAHTNTYFEIEAVNGVSDLSPGARQVYVAVTINQAAPSPVTNV 418
QY 450 MKERVLORSVQLSMOBEPHNGVITTEIKYKEDQREKRTYTLKTSASINNLKPGT 509
DB 419 KKGKIAKNSISLSWQPPDRPNGIILEYELKHEKDO-EISYTIKSKETTTBGLKPNAS 477
QY 510 VYVFOIRAVTAAGYNGYSPRLDVATLEASGKMFET--AVSSEQNPLYIIAIVAVAGT 566
DB 478 VYVFOIRARTPAAGYVFSRFE-----FETTPVFAASSDQSLPVIASVTYVG- 525
QY 567 IIVENVFGFTI-----GRR-----HCGYSKADQEDBE-LYFHS 600
DB 526 VILLAVVIGVLISGSCCECGGRASSLCAVAPILIRGYSKAKODPEEKMHFN 582
RESULT 13
AAB08665
ID AAB08665 standard; protein; 983 AA.
XX
XX AAB08665;
AC
XX
XX 02-JAN-2001 (first entry)
DT
XX
XX Amino acid sequence of a human EphA3 HLA class II-binding peptide.
XX
XX EphA3; HLA class II-binding peptide; human leukocyte antigen; antigen;
XX CD4+ T lymphocyte; tumour associated gene; vaccine.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Binding-site 1..9
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 47..55
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 103..111
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 149..157
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 168..176
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 459..467
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 554..562
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 558..566
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 565..573
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 589..597
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 656..664
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 675..683
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 683..691
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 727..735
FT Binding-site /note= "HLA class I binding motif"
FT Binding-site 788..796

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FT /note= "HLA class I binding motif"
FT Binding-site 895..903
FT /note= "HLA class I binding motif"
FT Binding-site 929..937
FT /note= "HLA class I binding motif"
XX
XX MO200050589-A1.
XX
XX 31-AUG-2000.
XX
XX 18-FEB-2000; 2000MO-US004326.
XX
XX 22-FEB-1999; 99US-0121170P.
XX 08-OCT-1999; 99US-0158566P.
XX
XX (LUDM-) LUDWIG INST CANCER RES.
XX
XX Chiari R, Coulie P, Boon-Falleur T;
XX WPI; 2000-572089/53.
XX N-PSDB; AAA64458.
XX
XX Novel tyrosine kinase receptor, EphA3 human leukocyte antigen (HLA) class
XX II binding peptide and nucleic acid encoding the receptor, useful for
XX diagnosing and treating conditions characterized by expression of EphA3
XX gene.
XX
XX Claim 1; Page 81-83; 107pp; English.
XX
XX The present sequence represents a EphA3 HLA (human leukocyte antigen)
XX class II-binding peptide. EphA3 antigens, when presented by an antigen
XX presenting cell having a HLA class II molecule, effectively induce
XX activation and proliferation of CD4+ T lymphocytes. EphA3 is a tumour
XX associated gene. EphA3 HLA binding peptides are used for selectively
XX enriching a population of T lymphocytes. The peptides are also used for
XX diagnosing a disorder characterized by EphA3 or EphA3 HLA binding peptide
XX expression. The peptides are also used to treat a disorder characterized
XX by EphA3 expression. The EphA3 binding peptides are useful in producing
XX vaccines and antibody
XX
XX Sequence 983 AA;
XX
XX Query Match 53.8%; Score 1796; DB 3; Length 983;
XX Best Local Similarity 57.6%; Pred. No. 1,4e-150;
XX Matches 329; Conservative 102; Mismatches 128; Indels 12; Gaps 5;
XX
XX 28 QAAKEVLLDLSKAOQTELEWISSPPSGMEISGLDENTYPIRTYQVCVQNEPNQNNWLRT 87
XX 25 QPSNEVNLDSKTIQGLGWSYPSHGMEISGVDEHYTPRTYQVCVNDHDSQNNWLRT 84
XX
XX 88 NMISKGAORIFVLEKTTLDQNSLPGVLGCTKTFNLVYETPYDGRNIREMLYKID 147
XX 85 NMVPRNSAQKIYELKFTLDQNSIPVLGCTKTFNLVYESDDHGVKEREHQFTKID 144
XX
XX 148 TIAADEFTTGDDGERKMLNTEVREIGPLSKGFYLAFOVAGACIALSVKYYKKCMT 207
XX 145 TIAADEFTTGDDGERKMLNTEVREIGPLSKGFYLAFOVAGACIALSVKYYKKCMT 204
XX
XX 208 IVENLAVPPTVTGSEFSSSLVEVAGTCVSSAEEBAENSPRMHGAGSEWLPIGKICCA 267
XX 205 TVKKILAFPTDTPV-MDSQSLVEVAGTCVSSAEEBAENS--EDPPRYCSTEGEWLPIGKICCA 261
XX
XX 268 GYQOKGPTCEPCGRFRFKSSQDLCGRCPHSHSDSGSRCEGQGYRPAADPPRYA 327
XX 262 GYBERGFMCAQCRGPFKALDGNMKCAKCPHSHSTQDGSNKCENNYFAADDPSPMA 321
XX
XX 328 CTRPPASPOLIFINOTVTSLEWSPPADNGRADVTYRIICKRCSEOGCEVPCGSNIG 387
XX 322 CTRPPSSPRNVISINETSVLIDWSWPLDIDGKRDVFNITCKCKGNMKCEFCFSNVR 381
XX
XX 388 YMPQQTGLENDYVTVMDLAHANTTVEEAVNGVSDLSRSQRLFAVVSITTTGAAPQVS 447
XX 382 FLPRQGLTNTVTVTVDLHAHTNTTPEIDAVNGVSELSPPRQFAAVSITTTGAAPSVL 441

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XX
XX 448 GWMKERVLSORSVQSWOEPHPNGVITEYEIKYKQDERTYSTLKSTASINLKP 507
XX 442 TIKDRSRNSISLSWOPHPNGIILDEVKTYKEQOETSTYLARGTNVTLSLKP 501
XX
XX 508 GTVYVFOIRAVTAAGYGNYSPLDVAITLEASGCMFEATVSSBQNPVILIAVAVAGTI 567
XX 502 DTIVVFOIRARTAGVGTNSRKEFEFTSP-----DSFISGSSQVNMIAISAVAIL 554
XX
XX 568 ILVPMVGFIIIGRRHCGYSKADQGBDELYF 598
XX 555 LLTVVYI-VLIG-RFCGYKSKGADKRIHF 583
XX
XX RESULT 14
XX ID AAB08666 standard; protein; 983 AA.
XX AC AAB08666;
XX DT 02-JAN-2001 (first entry)
XX
XX A human EphA3 HLA class II-binding peptide.
XX
XX EphA3; HLA class II-binding peptide; human leukocyte antigen; antigen;
XX CD4+ T lymphocyte; tumour associated gene; vaccine.
XX
XX Homo sapiens.
XX
XX MO200050589-A1.
XX
XX 31-AUG-2000.
XX
XX 18-FEB-2000; 2000MO-US004326.
XX
XX 22-FEB-1999; 99US-0121170P.
XX 08-OCT-1999; 99US-0158566P.
XX
XX (LUDM-) LUDWIG INST CANCER RES.
XX
XX Chiari R, Coulie P, Boon-Falleur T;
XX WPI; 2000-572089/53.
XX N-PSDB; AAA64458.
XX
XX Novel tyrosine kinase receptor, EphA3 human leukocyte antigen (HLA) class
XX II binding peptide and nucleic acid encoding the receptor, useful for
XX diagnosing and treating conditions characterized by expression of EphA3
XX gene.
XX
XX Claim 1; Page 88-90; 107pp; English.
XX
XX The present sequence represents a EphA3 HLA (human leukocyte antigen)
XX class II-binding peptide. EphA3 antigens, when presented by an antigen
XX presenting cell having a HLA class II molecule, effectively induce
XX activation and proliferation of CD4+ T lymphocytes. EphA3 is a tumour
XX associated gene. EphA3 HLA binding peptides are used for selectively
XX enriching a population of T lymphocytes. The peptides are also used for
XX diagnosing a disorder characterized by EphA3 or EphA3 HLA binding peptide
XX expression. The peptides are also used to treat a disorder characterized
XX by EphA3 expression. The EphA3 binding peptides are useful in producing
XX vaccines and antibody
XX
XX Sequence 983 AA;
XX
XX Query Match 53.8%; Score 1796; DB 3; Length 983;
XX Best Local Similarity 57.6%; Pred. No. 1,4e-150;
XX Matches 329; Conservative 102; Mismatches 128; Indels 12; Gaps 5;
XX
XX 28 QAAKEVLLDLSKAOQTELEWISSPPSGMEISGLDENTYPIRTYQVCVQNEPNQNNWLRT 87
XX 25 QPSNEVNLDSKTIQGLGWSYPSHGMEISGVDEHYTPRTYQVCVNDHDSQNNWLRT 84

```



```

QY 481 YEKDQERITYSTLTKTSTASINNLRKGTYYVFOIRAVTAAGYNSPRLDVATLEBASG 540
    |||
Db 481 YEKDQERITYSTLTKTSTASINNLRKGTYYVFOIRAVTAAGYNSPRLDVATLEBASG 540
QY 541 KMEFATAVSSEQNPVILIAVAVAGTILVFMVFGFIIIGRRHCGYSKADQEGDEELYFHS 600
    |||
Db 541 KMEFATAVSSEQNPVILIAVAVAGTILVFMVFGFIIIGRRHCGYSKADQEGDEELYFHS 600
QY 601 LVTNEHLSVL 610
    |||
Db 601 LVTNEHLSVL 610

```

RESULT 2

```

JC5673
receptor tyrosine kinase (EC 2.7.1.-) Edb-td1 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 07-May-1999
C/Accession: J05673
R:Alukder, A.H.; Muramatsu, T.; Kaneda, N.
Cell Struct. Funct. 22, 477-485, 1997
A>Title: A novel truncated variant form of Edb/MDK1 receptor tyrosine kinase is expressed
A:Reference number: J05672; MUID:98035156; PMID:9368721
A:Accession: J05673
A:Molecule type: mRNA
A:Residues: 1-605 <TAL>
A:Experimental source: embryo
C:Comment: This enzyme plays a regulatory role during neural development and embryogenesis
C/Keywords: brain; phosphotransferase
F:/30/Domain: signal sequence #status predicted <SIG>
F:/31-605/Product: receptor tyrosine kinase Edb-td1 #status predicted <MAT>
F:/31-548/Domain: extracellular #status predicted <EXT>
F:/31-438/Domain: fibronectin type III repeat <FN2>
F:/441-534/Domain: fibronectin type III repeat <FN2>
F:/549-574/Domain: transmembrane #status predicted <TM>

```

```

Query Match 98.8%; Score 3203.5; DB 2; Length 605;
Best Local Similarity 99.2%; Pred. No. 8.3e-224;
Matches 605; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

```

```

QY 1 MVVQTRPSPWIIICYLWLGFAHTGEAOAKAYLLDLSKAQOTLEWISSPPSGWEEISG 60
    |||
Db 1 MVVQTRPSPWIIICYLWLGFAHTGEAOAKAYLLDLSKAQOTLEWISSPPSGWEEISG 60
QY 61 LDENYPIRTYQVCQVMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCNSLPGVIGTCK 120
    |||
Db 61 LDENYPIRTYQVCQVMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCNSLPGVIGTCK 120
QY 121 EFTNLYYETDYGTRNIRENLVYKIDTIADESFTQDGERKMKLNTVREIGPLSKK 180
    |||
Db 121 EFTNLYYETDYGTRNIRENLVYKIDTIADESFTQDGERKMKLNTVREIGPLSKK 180
QY 181 GFPLAFQDVACIALVSVKYKKWTVENLAVFPDVTGSEFSSLVEVRGTCVSAAE 240
    |||
Db 181 GFPLAFQDVACIALVSVKYKKWTVENLAVFPDVTGSEFSSLVEVRGTCVSAAE 240
QY 241 EAENSFRMHCSAGEWLVPIGKICAKGYQOKDTEPCGRRFYKSSODLQSCRPTHS 300
    |||
Db 241 EAENSFRMHCSAGEWLVPIGKICAKGYQOKDTEPCGRRFYKSSODLQSCRPTHS 300
QY 301 FSDREGSSRCECDGYRASPDPYACTRPPSAPNLLFNINQTVSLFMSPPADNGR 360
    |||
Db 301 FSDREGSSRCECDGYRASPDPYACTRPPSAPNLLFNINQTVSLFMSPPADNGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTVMDLAAHAYTEVEAVNG 420
    |||
Db 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTVMDLAAHAYTEVEAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGQAAPSOVSGWKEKRVLQSVQSWQEPHNPVITTEYEIKY 480
    |||
Db 421 VSDLSRSQRLFAAVSITTTGQAAPSOVSGWKEKRVLQSVQSWQEPHNPVITTEYEIKY 480
QY 481 YEKDQERITYSTLTKTSTASINNLRKGTYYVFOIRAVTAAGYNSPRLDVATLEBASG 540
    |||

```

```

Db 481 YEKDQERITYSTLTKTSTASINNLRKGTYYVFOIRAVTAAGYNSPRLDVATLEBAS- 539
    |||
QY 541 KMEFATAVSSEQNPVILIAVAVAGTILVFMVFGFIIIGRRHCGYSKADQEGDEELYFHS 600
    |||
Db 540 ----ATAVSSEQNPVILIAVAVAGTILVFMVFGFIIIGRRHCGYSKADQEGDEELYFHS 595
QY 601 LVTNEHLSVL 610
    |||
Db 596 LVTNEHLSVL 605

```

RESULT 3

```

148614
developmental kinase 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I48614; S51742
R:Closek, T.; Millaer, B.; Ullrich, A.
Oncogene 9, 97-108, 1995
A>Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a novel
A:Reference number: I48611
A:Accession: I48614
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-626 <RES>
A/Cross-references: UNIPROT:Q61772; EMBL:X79084; NID:9607137; PID:CAA55689.1; PID:960713;

```

```

Query Match 98.6%; Score 3199; DB 2; Length 626;
Best Local Similarity 100.0%; Pred. No. 1.8e-223;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MVVQTRPSPWIIICYLWLGFAHTGEAOAKAYLLDLSKAQOTLEWISSPPSGWEEISG 60
    |||
Db 1 MVVQTRPSPWIIICYLWLGFAHTGEAOAKAYLLDLSKAQOTLEWISSPPSGWEEISG 60
QY 61 LDENYPIRTYQVCQVMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCNSLPGVIGTCK 120
    |||
Db 61 LDENYPIRTYQVCQVMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCNSLPGVIGTCK 120
QY 121 EFTNLYYETDYGTRNIRENLVYKIDTIADESFTQDGERKMKLNTVREIGPLSKK 180
    |||
Db 121 EFTNLYYETDYGTRNIRENLVYKIDTIADESFTQDGERKMKLNTVREIGPLSKK 180
QY 181 GFPLAFQDVACIALVSVKYKKWTVENLAVFPDVTGSEFSSLVEVRGTCVSAAE 240
    |||
Db 181 GFPLAFQDVACIALVSVKYKKWTVENLAVFPDVTGSEFSSLVEVRGTCVSAAE 240
QY 241 EAENSFRMHCSAGEWLVPIGKICAKGYQOKDTEPCGRRFYKSSODLQSCRPTHS 300
    |||
Db 241 EAENSFRMHCSAGEWLVPIGKICAKGYQOKDTEPCGRRFYKSSODLQSCRPTHS 300
QY 301 FSDREGSSRCECDGYRASPDPYACTRPPSAPNLLFNINQTVSLFMSPPADNGR 360
    |||
Db 301 FSDREGSSRCECDGYRASPDPYACTRPPSAPNLLFNINQTVSLFMSPPADNGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTVMDLAAHAYTEVEAVNG 420
    |||
Db 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTVMDLAAHAYTEVEAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGQAAPSOVSGWKEKRVLQSVQSWQEPHNPVITTEYEIKY 480
    |||
Db 421 VSDLSRSQRLFAAVSITTTGQAAPSOVSGWKEKRVLQSVQSWQEPHNPVITTEYEIKY 480
QY 481 YEKDQERITYSTLTKTSTASINNLRKGTYYVFOIRAVTAAGYNSPRLDVATLEBASG 540
    |||
Db 481 YEKDQERITYSTLTKTSTASINNLRKGTYYVFOIRAVTAAGYNSPRLDVATLEBASG 540
QY 541 KMEFATAVSSEQNPVILIAVAVAGTILVFMVFGFIIIGRRHCGYSKADQEGDEELYFHS 600
    |||
Db 541 KMEFATAVSSEQNPVILIAVAVAGTILVFMVFGFIIIGRRHCGYSKADQEGDEELYFHS 600
QY 601 L 601

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Db 601 L 601

RESULT 4

JCS672

receptor tyrosine kinase (EC 2.7.-.-) Etk precursor - mouse

N:Alternate names: developmental kinase 1

C:Species: Mus musculus (house mouse)

C:Date: 20-Nov-1997 #sequence revision 20-Nov-1997 #text_change 09-Jul-2004

C:Accession: JCS672; 148611; S51740

R:Translator: A.H.; Muramatsu, T.; Kaneda, N.

Cell Struct. Funct. 22, 477-485, 1997

A:Title: A novel truncated variant form of Etk/MDK1 receptor tyrosine kinase is expressed

A:Reference number: JCS672; MUID:98035156; PMID:9368721

A:Accession: JCS672

A:Molecule type: mRNA

A:Residues: 1-998 <TAL>

A:Cross-references: UNIPROT:Q61772

A:Experimental source: embryo

R:Closest, T.; Millauer, B.; Ullrich, A.

Oncogene 9, 97-108, 1995

A:Title: Identification of alternatively spliced mRNAs encoding variants of MDK1, a novel

A:Reference number: 148611

A:Accession: 148611

A:Molecule type: translated from GB/EMBL/DBJ

A:Status: preliminary

A:Residues: 1-998 <RES>

A:Cross-references: EMBL:X79082; NID:9607133; PIDN:CAA55687.1; PID:9607134

C:Comment: This enzyme plays a role during development involving differentiation and pro

C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat h

C:Keywords: ATP; brain; phosphotransferase; transmembrane protein

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-998/Product: receptor tyrosine kinase Etk #status predicted <MAT>

F:31-553/Domain: extracellular #status predicted <EXT>

F:331-438/Domain: fibronectin type III repeat <FN1>

F:441-534/Domain: fibronectin type III repeat <FN2>

F:554-579/Domain: transmembrane #status predicted <TM>

F:631-697/Domain: protein kinase homology <KIN>

F:639-647/Region: protein kinase ATP-binding motif

F:920-986/Domain: SAM homology <SAM>

Query Match 98.4%; Score 3191; DB 2; Length 998;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MVTQTRPPSWIILCYIWLGFPAHTGEAQAKEVLLDSKAQOTLEWISSPPSGMEETISG 60
DB 1 MVTQTRPPSWIILCYIWLGFPAHTGEAQAKEVLLDSKAQOTLEWISSPPSGMEETISG 60
QY 61 LDEYVTPIRTYQVQVWEPNPNMNLRTNWSKGAQRIFVELKFTLDCNSLPVLTGTC 120
DB 61 LDEYVTPIRTYQVQVWEPNPNMNLRTNWSKGAQRIFVELKFTLDCNSLPVLTGTC 120
QY 121 ETEFLYYETDYPDGRNIRENLVYKIDITIADESFTQDGERKMKLNTVEIREIGPLSK 180
DB 121 ETEFLYYETDYPDGRNIRENLVYKIDITIADESFTQDGERKMKLNTVEIREIGPLSK 180
QY 181 GFYLAPODVACIALVSVKYYKKCWITVENLAVFPDVTGSESSSLVEVRGTCVSSAEE 240
DB 181 GFYLAPODVACIALVSVKYYKKCWITVENLAVFPDVTGSESSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPMHCSABEEMVLPVIGKCI CKAGYQOKGDTCEPCGRPFKSSSODLQSCRCPHS 300
DB 241 EAENSPPMHCSABEEMVLPVIGKCI CKAGYQOKGDTCEPCGRPFKSSSODLQSCRCPHS 300
QY 301 FSDREGSSRCCEGEGYRAPSDPYVACTRPPSAPOULIFININQTVLSLEMSPADNGR 360
DB 301 FSDREGSSRCCEGEGYRAPSDPYVACTRPPSAPOULIFININQTVLSLEMSPADNGR 360
QY 361 NDVTYRILCKRCMSWEGECVPCGSNIGYMPQOTGLEBNYTVMDLAAHYATFEVAVNG 420
DB 361 NDVTYRILCKRCMSWEGECVPCGSNIGYMPQOTGLEBNYTVMDLAAHYATFEVAVNG 420
```

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QY 421 VSDLSRSQRLFAAVSITTGQAAPSVGWMKERVLRQSVLSWQEPHPNGVITEYIKY 480
DB 421 VSDLSRSQRLFAAVSITTGQAAPSVGWMKERVLRQSVLSWQEPHPNGVITEYIKY 480
QY 481 YEKQRRERTYSTLTKTSASINNLKPGTYVVPQIRAVTAAGYGNVSPRLDVALLEBASG 540
DB 481 YEKQRRERTYSTLTKTSASINNLKPGTYVVPQIRAVTAAGYGNVSPRLDVALLEBASG 540
QY 541 KMFEPATVSSBONPVIIIAVAVAGTIIIVFMVGFIIGRHCGYSKADQDEBELYFH 599
DB 541 KMFEPATVSSBONPVIIIAVAVAGTIIIVFMVGFIIGRHCGYSKADQDEBELYFH 599
```

RESULT 5

158351

receptor protein-tyrosine kinase - human

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: 158351

R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher,

Oncogene 10, 897-905, 1995

A:Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty-

A:Reference number: 158351; MUID:95206782; PMID:7898931

A:Accession: 158351

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-998 <RES>

A:Cross-references: UNIPROT:Q15375; GB:J36642; NID:9551607; PIDN:AAA74243.1; PID:9551608

C:Genetics:

A:Gene: HEK11

C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat h

C:Keywords: ATP; transmembrane protein

F:631-697/Domain: protein kinase homology <KIN>

F:639-647/Region: protein kinase ATP-binding motif

F:920-986/Domain: SAM homology <SAM>

Query Match 96.8%; Score 3139; DB 2; Length 998;
Best Local Similarity 97.7%; Pred. No. 7.5e-219;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MVTQTRPPSWIILCYIWLGFPAHTGEAQAKEVLLDSKAQOTLEWISSPPSGMEETISG 60
DB 1 MVTQTRPPSWIILCYIWLGFPAHTGEAQAKEVLLDSKAQOTLEWISSPPSGMEETISG 60
QY 61 LDEYVTPIRTYQVQVWEPNPNMNLRTNWSKGAQRIFVELKFTLDCNSLPVLTGTC 120
DB 61 LDEYVTPIRTYQVQVWEPNPNMNLRTNWSKGAQRIFVELKFTLDCNSLPVLTGTC 120
QY 121 ETEFLYYETDYPDGRNIRENLVYKIDITIADESFTQDGERKMKLNTVEIREIGPLSK 180
DB 121 ETEFLYYETDYPDGRNIRENLVYKIDITIADESFTQDGERKMKLNTVEIREIGPLSK 180
QY 181 GFYLAPODVACIALVSVKYYKKCWITVENLAVFPDVTGSESSSLVEVRGTCVSSAEE 240
DB 181 GFYLAPODVACIALVSVKYYKKCWITVENLAVFPDVTGSESSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPMHCSABEEMVLPVIGKCI CKAGYQOKGDTCEPCGRPFKSSSODLQSCRCPHS 300
DB 241 EAENSPPMHCSABEEMVLPVIGKCI CKAGYQOKGDTCEPCGRPFKSSSODLQSCRCPHS 300
QY 301 FSDREGSSRCCEGEGYRAPSDPYVACTRPPSAPOULIFININQTVLSLEMSPADNGR 360
DB 301 FSDREGSSRCCEGEGYRAPSDPYVACTRPPSAPOULIFININQTVLSLEMSPADNGR 360
QY 361 NDVTYRILCKRCMSWEGECVPCGSNIGYMPQOTGLEBNYTVMDLAAHYATFEVAVNG 420
DB 361 NDVTYRILCKRCMSWEGECVPCGSNIGYMPQOTGLEBNYTVMDLAAHYATFEVAVNG 420
QY 421 VSDLSRSQRLFAAVSITTGQAAPSVGWMKERVLRQSVLSWQEPHPNGVITEYIKY 480
DB 421 VSDLSRSQRLFAAVSITTGQAAPSVGWMKERVLRQSVLSWQEPHPNGVITEYIKY 480
```


Db 608 PEEBKMHFH---NGHKL 622

RESULT 8

receptor tyrosine kinase Etk-1 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S49015; S51602
R/Misnomer: P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A/Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A/Reference number: S49015; MUID:94067777; PMID:7504232
A/Accession: S49015
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1005 <MA1>
A/Cross-references: UNIPROT:P54757; EMBL:S68024
A/Note: the authors translated the codon GAC for residue 170 as Glu
A/Accession: S51602
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-305, 'G', 359-1005 <MA2>
A/Cross-references: EMBL:S68026
A/Note: the authors translated the codon GAC for residue 170 as Glu
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C/Keywords: ATP; transmembrane protein
F/675-941/Domain: protein kinase homology <KIN>
F/683-691/Region: protein kinase ATP-binding motif

Query Match 56.2%; Score 1821; DB 2; Length 1005;
Best Local Similarity 54.6%; Pred. No. 1.6e-123;
Matches 350; Conservative 97; Mismatches 138; Indels 56; Gaps 11;

QY 6 RFEWITLCY-----IW-----LLGPAHTEAOAAKEVLLDSKAQOTLEWISPPSG 54
DB 25 RVPASLKGVSAPLKGPLMCTLLCALRTLLASPSNEVNLDRVTVGDIQWIAFPNG 84
QY 55 WEETSGIDENYTPRTYOVQVMEPNQNNMLRTNWSKGNQRI FVELKFTLRDQNSLP 114
DB 85 WEETSGIDENYTPRTYOVQVMEPNQNNMLRTNWSKGNQRI FVELKFTLRDQNSLP 144
QY 115 VLGTCKETFNLYETDYDTGRNIRENLYVKIDITIADESFTQDGLGRKKMLTEVREI 174
DB 145 GLGTCKETFNLYETDYDTGRNIRENLYVKIDITIADESFTQDGLGRKKMLTEVREI 204
QY 175 GLPSKGFYLAFOVGAICIALVSRYKVCWTIVENLAVFPDVTGSEFSSLYVNGTC 234
DB 205 GLPSKGFYLAFOVGAICIALVSRYKVCWTIVENLAVFPDVTGSEFSSLYVNGTC 264
QY 235 VSSAEBAENSBRMGCAEGEWLVPICGICKAGYQOKGTCPCGRFRFYSSQDLOCS 294
DB 265 VN--HSVTDPPKMGCAEGEWLVPICGICKAGYQOKGTCPCGRFRFYSSQDLOCS 322
QY 295 RCPHTSFDEGSSRCCEGDYRAPSDPYVACTRPPSPAPQNLIFINQTVLSLEWSP 354
DB 323 KCPHSTHBAASISVCYCKDYPRESPPYMACTRPPSPAPQNLISVNETSVLEWIP 382
QY 355 ADNGRNDVYRIILCKRCSWEGECVPCGSNIGYMPQOTGLENDYVTVMDLAAHYTFE 414
DB 383 ADTGCGADVSYIILCKRCSWEGECVPCGSNIGYMPQOTGLENDYVTVMDLAAHYTFE 442
QY 415 VEAANGVSDLSRSRLRFAAVSITTGGAAPSOVSGWKEKRVLRVSQVLSMOEBHPNGVIT 474
DB 443 IEAANGVSDLSRSRLRFAAVSITTGGAAPSOVSGWKEKRVLRVSQVLSMOEBHPNGVIT 502
QY 475 EYEIKYEQDREKTYSLTKTSASINLKPCTVYVFOIRATYAGYGYSPRLDYAT 534
DB 503 EYEIKYEQDREKTYSLTKTSASINLKPCTVYVFOIRATYAGYGYSPRLDYAT 558
QY 535 LEEASGKFEATYV---SSBONPVYIIIAVAVAGTIIILVFNVPFGII-----GRR- 581
DB 559 -----FETTPVFGASNDQSIPIIGSVTVGVILLAVMI-GFLLSGSCCECGCGRAS 609

QY 582 -----HCGSKADQEGDEE-LYFSLVTNHELSV 609
DB 610 SLCAVAHPSLIMKRGYSKAKQDPEEBKMHF---NGHKL 646

RESULT 9

receptor-tyrosine-protein-tyrosine kinase Csk7, long splice form - chicken
C/Species: Gallus gallus (chicken)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: 150615; 150616; 150614
R/Siever, D.A.; Verderame, M.F.
Gene 148, 219-226, 1994
A/Title: Identification of a complete Csk7 receptor protein tyrosine kinase coding seque
A/Reference number: 150614; MUID:95047425; PMID:7958948
A/Accession: 150615
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1013 <SIE>
A/Cross-references: UNIPROT:P54755; EMBL:U03910; NID:9555617; PIDN:AAB60612.1; PID:95556
A/Accession: 150616
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-572, 'R', 596-1013 <S12>
A/Cross-references: EMBL:U03910; NID:9555617; PIDN:AAB60613.1; PID:9555619
A/Accession: 150614
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-279, 444-572, 'R', 596-1013 <S13>
A/Cross-references: EMBL:U03910; NID:9555617; PIDN:AAB60614.1; PID:9555620
C/Genetics:
A:Gene: Csk7
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C/Keywords: alternative splicing; ATP; transmembrane protein
F/649-915/Domain: protein kinase homology <KIN>
F/657-665/Region: protein kinase ATP-binding motif
F/938-1004/Domain: SAM homology <SAM>

Query Match 55.6%; Score 1802; DB 2; Length 1013;
Best Local Similarity 53.3%; Pred. No. 3.9e-122;
Matches 347; Conservative 96; Mismatches 137; Indels 48; Gaps 10;

QY 8 PSW--ILICYTWLLGPAHTEAOAAKEVLLDSKAQOTLEWISPPSGMEISGLDENY 65
DB 15 PWTCLLCAALNSLSPG-----SEVNLDRSTWGDGLIAYPKNGEIEGVENY 69
QY 66 TPRTYOVQVMEPNQNNMLRTNWSKGNQRI FVELKFTLRDQNSLPGLGTCKETFN 125
DB 70 APHTYOVQVMEPNQNNMLRTNWSKGNQRI FVELKFTLRDQNSLPGLGTCKETFN 129
QY 126 YYETDYDTGRNIRENLYVKIDITIADESFTQDGLGRKKMLTEVREIPLSKGYLA 185
DB 130 YFESDDEDRNIRENLYVKIDITIADESFTQDGLGRKKMLTEVREIPLSKGYLA 189
QY 186 FQDVGAICIALVSRYKVCWTIVENLAVFPDVTGSEFSSLYVNGTCV-SAEBAEN 244
DB 190 FQDVGAICIALVSRYKVCWTIVENLAVFPDVTGSEFSSLYVNGTCV-SAEBAEN 247
QY 245 SPRMGCAEGEWLVPICGICKAGYQOKGTCPCGRFRFYSSQDLOCSRCPHTSFSR 304
DB 248 -PKMGCAEGEWLVPICGICKAGYQOKGTCPCGRFRFYSSQDLOCSRCPHTSFSR 306
QY 305 EGSSRCCEGTYRAPSDPYVACTRPPSPAPQNLIFINQTVLSLEWSPRPDNGRVDY 364
DB 307 EASTSCLEEHYFRESPPYMACTRPPSPAPQNLISVNETSVLEWIPPDVTGGRDVS 366
QY 365 YRIILCKRCSWEGECVPCGSNIGYMPQOTGLENDYVTVMDLAAHYTFEVAANGVSD 424
DB 367 YRIILCKRCSWEGECVPCGSNIGYMPQOTGLENDYVTVMDLAAHYTFEVAANGVSD 426
QY 425 SRSGRLFAAVSITTGGAAPSOVSGWKEKRVLRVSQVLSMOEBHPNGVITYEIKYKED 484

Db 427 NPGARQVSVNVTNNQAAPEPVSSVKKGKTTKNSISLSWQEPDRPNCIILLYEIKYEKD 486
 QY 485 QRERTYSTLTKSTASINNLKPGTVVYFOIRAVTAAGYGNYSPLDVAITLEASGKMF 544
 Db 487 Q-ETSYTIISKETAIADGKPGSAVYFOIRAVTAAGYGNYSPLDVAITLEASGKMF 537
 QY 545 ATAVSSQONVILIAVAVAGTITLLVPMVPGFIIGRR-----H 582
 Db 538 VLAASSQSQSIPII-VVSVTVGVILAVIGFLLSGSCDHCWMASSLRVAVPSLIWR 596
 QY 583 CGYSKADQEGDEE-LYFHSVLTNEHLSV 609
 Db 597 CGYSKADQEGDEE-LYFHSVLTNEHLSV 620

RESULT 10

A38224
 protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C/Accession: A38224; B38224
 R/Wicks, I.P.; Wilkerson, D.; Salvaris, E.; Boyd, A.W.
 Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
 A/Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed
 A/Reference number: A38224; MUID:92179233; PMID:1311845
 A/Accession: A38224
 A/Molecule type: mRNA
 A/Residues: 1-983 <WIC>
 A/Cross-references: UNIPROT:P29320; GB:M83941; NID:g183931; PIDN:AAA5663.1; PID:g183932
 A/Experimental source: pre-B-cell leukemia cell line LK63
 A/Note: sequence extracted from NCBI database (NCBI:86627)
 A/Accession: B38224
 A/Molecule type: protein
 A/Residues: 21-39/810-860 <M12>
 C/Suprafamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C/Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
 F:1/20/Domain: signal sequence #status predicted <SIG>
 F:21-983/Product: protein-tyrosine kinase hek #status experimental1 <MAT>
 F:542-565/Domain: transmembrane #status predicted <TM>
 F:619-885/Domain: protein kinase homology <KIN>
 F:627-635/Region: protein kinase ATP-binding motif
 F:232,337,391,404,493/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 55.5%; Score 1799; DB 2; Length 983;

Best Local Similarity 57.0%; Pred. No. 6.2e-122;
 Matches 332; Conservative 103; Mismatches 131; Indels 16; Gaps 6;

QY 28 QAAKEVLLDSKAQQTLEWISSPGMEISGLDENYPIRTYOVQWENPNNMLRT 87
 Db 25 QPSNEVALLDSKTIQGLGMIYSPHSGMEISGVDEHYPIRTYOVQWENPNNMLRT 84
 QY 88 NMISKGAQRIFVELKFTLRDNCNLPGLGTCKETFNLYYETDYDGRNIRENLYYKID 147
 Db 85 NMPVPRNSAQKITVELKFTLRDNCNLPGLGTCKETFNLYYETDYDGRNIRENLYYKID 144
 QY 148 TIAADESFTQDGERMKLNTVEIREIGPLSKGFIYAFODVACIALVSVKVYKKCW 207
 Db 145 TIAADESFTQDGERMKLNTVEIREIGPLSKGFIYAFODVACIALVSVKVYKKCW 204
 QY 208 IVENLAVFPTVYSESSSLVEVRGTVSSAAEEAENSPPMHGASABEMLVPIGKIC 267
 Db 205 TVKNLAFPTVYSESSSLVEVRGTVSSAAEEAENSPPMHGASABEMLVPIGKIC 261
 QY 268 GYOQKQCEPCGRRFYKSSSODLQCRPCTHSPFSDGSSRCCEDEGYVRAADPPYVA 327
 Db 262 GYERGERGACACRGFKALDGNMKKACPFHSTQDGSNCRCEENYVRADKDPSPMA 321
 QY 328 CTTPPSAPQULIFININOTVLSLEKSPADNGRNDVYRILCKRCSWEGECVPCGSNIG 387
 Db 322 CTTPPSAPQULIFININOTVLSLEKSPADNGRNDVYRILCKRCSWEGECVPCGSNIV 381
 QY 388 YMGQOQGLDENYVWMLLAHANYTPEVEAVNGVSDLSRQRLPAVNSITTGGAAPQVS 447

Db 382 FLPRQGLNTVYVTDLLAHNTYFEIDAANGVSELSPPEPPAAVSTTNOAAPSVL 441
 QY 448 GWAKERVLRQSVOLSWQEPHPNGVITEYEIKYEKQDERTYSTLTKSTASINNLKP 507
 Db 442 TIKKQDTSRNSISLSWQEPHPNGVITEYEIKYEKQDERTYSTLTKSTASINNLKP 501
 QY 508 GTTYVFOIRAVTAAGYGNYSPLDVAITLEASGKMEATRAVSSQNPVILIAVAVAGT 567
 Db 502 DTYVFOIRAVTAAGYGNYSPLDVAITLEASGKMEATRAVSSQNPVILIAVAVAGT 554
 QY 568 ILVPMVPGFIIGRRHCGSKADQEGDEELYFHSVLTNEHLSV 609
 Db 555 LITVTVY-VLIG-RFCGYKSKGADKRIHF-----GNGLKL 590

RESULT 11

A15149
 receptor tyrosine kinase - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C/Accession: I51549
 R/Wimings, R.S.; Sargent, T.D.
 Mech. Dev. 46, 219-229, 1994
 A/Title: Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, has 1c
 A/Reference number: I51549; MUID:95001564; PMID:7918105
 A/Accession: I51549
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-985 <MIN>
 A/Cross-references: UNIPROT:Q91694; GB:I26099; NID:g416402; PIDN:AAA64464.1; PID:g416403
 A/Genetic:
 A/Gene: Pag
 C/Suprafamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C/Keywords: ATP; transmembrane protein
 F:618-884/Domain: protein kinase homology <KIN>
 F:626-634/Region: protein kinase ATP-binding motif
 F:907-973/Domain: SAM homology <SAM>

Query Match 55.1%; Score 1788.5; DB 2; Length 985;

Best Local Similarity 57.6%; Pred. No. 3.6e-121;
 Matches 341; Conservative 93; Mismatches 145; Indels 13; Gaps 6;

QY 11 IILCYIMLGFATG-BAQAKVLLDSKAQQTLEWISSP-PSGMEISGLDENYPTI 68
 Db 8 ILFCGLFGCWAATGSRIPASEVTLTLDSSVQGLGMIASPLEGMEISGLDENYPTI 67
 QY 69 RTYOVQWENPNNMLRTNWIISKGAQRIFVELKFTLRDNCNLPGLGTCKETFNLYY 128
 Db 68 RTYOVQWENPNNMLRTNWIISKGAQRIFVELKFTLRDNCNLPGLGTCKETFNLYY 127
 QY 129 ETDYDGRNIRENLYYKIDTIAADESFTQDGERMKLNTVEIREIGPLSKGFIYAFOD 188
 Db 128 ESNNDKERFIRETYOYKIDTIAADESFTQDGERMKLNTVEIREIGPLSKGFIYAFOD 187
 QY 189 VGACIALVSVKVYKKCWITVENLAVFPTVYSESSSLVEVRGTVSSAAEEAENSPPM 248
 Db 188 VGACIALVSVKVYKKCWITVENLAVFPTVYSESSSLVEVRGTVSSAAEEAENSPPM 245
 QY 249 HCSAEGEMLVPIGKICCKAGYQKQDTPCEPCGRRFYKSSSODLQCRPCTHSPFSDGSS 308
 Db 246 YCGADEMLVPIGKICCKAGYQKQDTPCEPCGRRFYKSSSODLQCRPCTHSPFSDGSS 305
 QY 309 RCEDEGYVRAADPPYVACTRPPAPQULIFININOTVLSLEKSPADNGRNDVYRIL 368
 Db 306 SCTCDRGYVRAADPPYVACTRPPAPQULIFININOTVLSLEKSPADNGRNDVYRIL 365
 QY 369 CKRCSWEGECVPCGSNIGMPQDTLEDNYVWMLLAHANYTPEVEAVNGVSDLSRQ 428
 Db 366 CKRCSWEGECVPCGSNIGMPQDTLEDNYVWMLLAHANYTPEVEAVNGVSDLSRQ 425
 QY 429 RLFAVNSITTGGAAPQVSQWAKERVLRQSVOLSWQEPHPNGVITEYEIKYEKQD 488
 Db 426 DQAVSVTVITNOAAPSITVIOIPEKETTRHSVSLTPEPRANGVILEYKYEKQD 485

RESULT 14
I78844
receptor protein-tyrosine kinase - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change (9-Jul-2004
C/Accession: I78844
R/Fox, G.M.; Holte, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, I.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995
A/Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein-ty A/Reference number: 158351; MUID:95206782; PMID:7898931
A/Accession: I78844
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-986 <RES>
A/Cross-references: UNIPROT:P54764; GB:IJ3645; NID:g551613; PIDN:AAA74246.1; PID:g551614 C/Genetics:
A/Genes: HEK8
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h P,619-885/Domain: protein kinase homology <KIN>
F,908-974/Domain: SAM homology <SAM>

Query Match 53.5%; Score 1736.5; DB 2; Length 986;
Best Local Similarity 55.8%; Pred. No. 2,1e-117;
Matches 320; Conservative 107; Mismatches 133; Indels 3; Gaps 6;

QY 30 AKEVLLDSFAQOTLEWISSP-PSGMEISGLDENTYPTIRYQVCVMEPNQNNMLRTN 88
DB 28 ANEVTLIDSRVQGLGIMASPLEGMEVSIIMDEKPTPIRYQVCVME>SQNNMLRTD 87
QY 89 WISKGNQRIFFVLLKFTLRDCLSPGLGCKETFNLYETDYDGRNIRENLYKIDT 148
DB 88 WITREGQRYVIEIKFTLRDCLSPGLGCKETFNLYETDYDGRNIRENLYKIDT 147
QY 149 IADESFQDGLDERKMKLNTVEIREIGPLSKGFFYLAFOVGACIALVSYGVYKCKWTI 208
DB 148 IADESFQDGLDERKMKLNTVEIREIGPLSKGFFYLAFOVGACIALVSYGVYKCKWTI 207
QY 209 VENLAVPDITVTSSEFSSIVEVGTGVSSAEEAENSPRMCSAEGEWLVPIKCKICKAG 268
DB 208 VRLAOFPPDITVTSSEFSSIVEVGTGVSSAEEAENSPRMCSAEGEWLVPIKCKICKAG 265
QY 269 YQCKGDTCEPCGRFFYSSSSQDQCSRCPTHSFSDREGRSCCEQGYVAPDPPVAC 328
DB 266 HEBSRGECQCKIGYVYALSTDAICACPHYSVWEGATSCYCDRPFPRADDAAMPC 325
QY 329 TRPSPAPQNLIFINQTTVLSLEWSPADNGRNDVTYRIILCKRC-SWEOG3CVPCGSNIG 387
DB 326 TRPSPAPQNLIFINQTTVLSLEWSPADNGRNDVTYRIILCKRC-SWEOG3CVPCGSNIG 385
QY 388 YMPQGTGLENDYVTVMDLHANVTFEVAANGVSDLSRSQRLPAVSIITGQAAPSOVS 447
DB 386 YTPQOGLKTKTKYSITDLAHNTVTFEIMAVNGVSKPNPDOSVSTVITINDAASSIA 445
QY 448 GWNKERVLRQSVOLSMOEPHPNGVITVEIKYKEXDQRETYSTLKTSISAINMLKP 507
DB 446 LVPAKEVTRYSVALMLEPDRPGVILIEVVKYKEXDQRETYSTLKTSISAINMLKP 505
QY 508 GTVYVFEIRAVTAAGYNSPRLDVATLEBASGMFEATVSSSEONVILIAVAVAGTI 567
DB 506 LTVYVFEIRAVTAAGYNSPRLDVATLEBASGMFEATVSSSEONVILIAVAVAGTI 567
QY 568 IL-VFVWFGFIIGRRHCGYSKADQEGDEELVYH 599
DB 558 VLVVILIAFAVVISRRSKYSKAKOADEBEKHLN 590

RESULT 15
S78059
protein-tyrosine kinase (EC 2.7.1.112) Eph precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: S78059; S30505; I58366
R/Charney, P.

submitted to the EMBL Data Library, March 1992
A/Reference number: S78059
A/Accession: S78059
A/Molecule type: mRNA
A/Residues: 1-986 <CHA>
A/Cross-references: UNIPROT:Q03137; EMBL:X65138; NID:g54083; PIDN:CAA6266.1; PID:g54084 R/Gillard, H. Hebenstreit, P.; Nito, M.A.; Frain, M.; Walter, M.G.; Chastier, A.; Wilkinson, Oncogene 7, 2499-2506, 1992
A/Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in t A/Reference number: S30496; MUID:93096484; PMID:1281307
A/Accession: S30505
A/Molecule type: mRNA
A/Residues: 1-31,55-986 <GTL>
A/Cross-references: EMBL:X65138
C/Genetics:
A/Genes: Sek
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h C/Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase; t F,1-15/Domain: signal sequence #status predicted <SIG>
F,16-986/Product: protein-tyrosine kinase Eph #status predicted <KAT>
F,548-569/Domain: transmembrane #status predicted <TM>
F,619-885/Domain: protein kinase homology <KIN>
F,627-635/Region: protein kinase ATP-binding motif
F,908-974/Domain: SAM homology <SAM>
F,235,340,408,423/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.0%; Score 1718; DB 2; Length 986;
Best Local Similarity 54.0%; Pred. No. 4.5e-116;
Matches 321; Conservative 113; Mismatches 146; Indels 14; Gaps 7;

QY 10 WITLCYIMLIGFAHTG-ENQAKVLLDSKAQOTLEWISSP-PSGMEISGLDENTYPT 67
DB 7 FILFSLFGLICDVAVTSRYVPAVEVTLIDSRVQGLGIMASPLEGMEVSIIMDEKPT 66
QY 68 IRTYQVCVMEPNQNNMLRTNMTSKGNAORIFELKFTLRDCLSPGLGCKETFNLY 127
DB 67 IRTYQVCVMEPNQNNMLRTNMTSKGNAORIFELKFTLRDCLSPGLGCKETFNLY 126
QY 128 YETDYDGRNIRENLYKIDTIADESFTQGLDERKMKLNTVEIREIGPLSKGFFYLAFO 187
DB 127 YESDYNKERFIRSGQKGTDTIADESFTQGLDERKMKLNTVEIREIGPLSKGFFYLAFO 186
QY 188 DVGACIALVSVKYYKCKWTIENLAVPDITVTSSEFSSIVEVGTGVSSAEEAENS 247
DB 187 DVGACIALVSVKYYKCKWTIENLAVPDITVTSSEFSSIVEVGTGVSSAEEAENS 244
QY 248 MHCSAEGEWLVPIKCKICKAGYQCKGDTCEPCGRFFYSSSSQDQCSRCPTHSFSDREGS 307
DB 245 MHCSAEGEWLVPIKCKICKAGYQCKGDTCEPCGRFFYSSSSQDQCSRCPTHSFSDREGS 304
QY 308 SRCECEGYRAASDPVYACTRPPSPAPQNLIFINQTTVLSLEWSPADNGRNDVTYRI 367
DB 305 TSCTCDRGFPFRADDAAMPCSTRPPSPAPQNLIFINQTTVLSLEWSPADNGRNDVTYRI 364
QY 368 LCKRC-SWEOG3CVPCGSNIGYMPQGTGLENDYVTVMDLHANVTFEVAANGVSDLSR 426
DB 365 VCKRCGADGPSKCRPGSGVHYTPQNGLKTTRVSTJDLAHNTVTFEIMAVNGVSKPNP 424
QY 427 SORLPAVSIITGQAAPSOVSQVSGVWGMKERVLRQSVOLSMOEPHPNGVITVEIKYKEXDQ 486
DB 425 SPDSQSVVITVYVQAPSSIALVQAKETRYVALAMLEPDRNGVILIEVVKYKEXDQ 484
QY 487 ERTYSTLTKTSASINMLKPGTVVFPQIRAVTAAGYNSPRLDVATLEBASGMFEAT 546
DB 485 ERTYSTLTKTSASINMLKPGTVVFPQIRAVTAAGYNSPRLDVATLEBASGMFEAT 546
QY 547 AVSSEONPVILIAVAVAGTIIL-VFVWFGFIIGRRHCGYSKADQEGDEELVYH 599
DB 539 IIGDGANSTVLL--VSVSGSVLVVILIAFAVISRRSKYSKAKOADEBEKHLN 590

Search completed: August 23, 2005, 08:33:10
Job time : 18.2864 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 70.5744 Seconds

(without alignment)
4426.083 Million cell updates/sec

Title: US-10-073-064-3

Perfect score: 3243
Sequence: 1 MVVQTRPPSWILLCYIWLGL.....EGDELYFHSIVTNEHLSVL 610

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Uniprot_03.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3239	99.9	610	2 Q8CC52	Q8CC52 mus musculus
2	3191	98.4	998	2 EPB7 MOUSE	Q61772 mus musculus
3	3188	98.3	994	2 Q8R3B1	Q8R3B1 mus musculus
4	3187	98.3	998	2 Q8BSU8	Q8BSU8 mus musculus
5	3175	97.9	998	1 EPB7 RAT	P54759 ratu norv
6	3139	96.8	998	1 EPB7 HUMAN	Q15375 homo sapien
7	3126	96.4	593	2 Q8C7N2	Q8C7N2 mus musculus
8	3031.5	93.5	993	1 EPB7 CHICK	Q42422 gallus gall
9	1862.5	57.4	681	2 Q8C276	Q8C276 mus musculus
10	1821	56.2	1005	1 EPB5 RAT	P54757 ratu norv
11	1819	56.1	1037	1 EPB5 HUMAN	P54756 homo sapien
12	1802	55.6	984	2 Q8BRB1	Q8BRB1 mus musculus
13	1802	55.6	1013	1 EPB5 CHICK	P54755 gallus gall
14	1799	55.5	983	1 EPB3 HUMAN	P29320 homo sapien
15	1799	55.5	983	2 Q6P4R6	Q6P4R6 homo sapien
16	1798	55.4	984	2 Q8C3U1	Q8C3U1 mus musculus
17	1793.5	55.3	986	1 EPB4 XENLA	Q1845 xenopus lae
18	1790	55.2	969	2 Q7Z3F2	Q7Z3F2 homo sapien
19	1789.5	55.2	984	1 EPB3 RAT	Q06680 ratu norv
20	1788.5	55.1	985	1 EPB4 XENLA	Q91694 xenopus lae
21	1787.5	55.1	986	2 Q7ZVM7	Q7ZVM7 xenopus lae
22	1786.5	55.1	983	1 EPB3 CHICK	P29318 gallus gall
23	1786.5	55.1	983	1 EPB3 MOUSE	P29319 mus musculus
24	1747.5	53.9	986	1 EPB4 CHICK	Q07496 gallus gall
25	1739	53.6	538	2 Q8C9K6	Q8C9K6 mus musculus
26	1736.5	53.5	986	1 EPB4 HUMAN	P54764 homo sapien
27	1723	53.1	986	2 Q8OVZ2	Q8OVZ2 mus musculus
28	1718	53.0	986	1 EPB4 MOUSE	Q03137 mus musculus
29	1701.5	52.5	1005	1 EPB8 HUMAN	P29327 homo sapien
30	1695	52.3	1004	1 EPB6 MOUSE	Q09127 mus musculus
31	1662	51.2	948	1 EPB6 RAT	P54758 ratu norv

ALIGNMENTS

RESULT 1	Q8CC52	PRELIMINARY:	PRT:	610 AA.
AC	Q8CC52			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:330112M11 product:Bph receptor A7, full insert			
DE	sequence.			
GN	Name=Epha7;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;			
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;			
RA	Carninci P., Hayashizaki Y.;			
RT	"High-efficiency full-length cDNA cloning.";			
RL	Mech. Enzymol. 303:19-44(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;			
RC	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;			
RA	RIKEN FANTOM Consortium;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;			
RC	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";			
RL	Nature 420:563-573(2002).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;			
RC	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;			
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,			
RT	Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;			
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";			
RL	Genome Res. 10:1617-1630(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;			
RC	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;			
RA	Shibata K., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P.,			
RT	Kono H., Akiyama J., Nishi K., Kitsumi T., Tashiro H., Itoh M.,			
RT	Sun N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,			
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiyagi K.,			

32	1652	50.9	976	2 Q90ZM9	Q90ZM9 brachydanio
33	1651	50.9	1035	1 EPB6 MOUSE	Q62413 mus musculus
34	1631	50.3	981	1 EPB3 BRARE	Q3146 brachydanio
35	1625	50.1	927	2 Q99KX8	Q99KX8 mus musculus
36	1590	49.0	880	2 Q73879	Q73879 brachydanio
37	1496	46.1	1004	1 EPB2 CHICK	P28693 gallus gall
38	1477	45.5	994	1 EPB2 MOUSE	P29323 homo sapien
39	1475	45.5	1055	1 EPB2 HUMAN	Q66107 mus musculus
40	1474	45.5	1021	2 Q6GTQ7	Q6GTQ7 mus musculus
41	1470	45.3	987	1 EPB2 COTUA	Q90344 coturnix co
42	1465.5	45.2	1029	2 Q6P5F1	Q6P5F1 mus musculus
43	1458	45.0	279	2 Q8N368	Q8N368 homo sapien
44	1449	44.7	984	1 EPB1 RAT	P09759 ratu norv
45	1448.5	44.7	984	1 EPB1 HUMAN	P54762 homo sapien

RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Murakatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "IKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA Aachai J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii F., Imohani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Shibata H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Murakatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AK033903; BAC28509.1; -
 DR HSSP: P54763; INUK.
 DR MGD; MG195276; EphA7.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin receptor.
 DR InterPro: IPR003962; Ephrin subd.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN III-like.
 DR InterPro: IPR008979; Gal bind like.
 DR InterPro: IPR009030; Grow fac receptor.
 DR InterPro: IPR001426; Ykase receptor.
 DR Pfam: PF01404; Ephrin_1bd; 1.
 DR Pfam: PF00014; FNTPEI11.
 DR PRINTS; PR00014; FNTPEI11.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR SMART; SM00615; EPH_1bd; 1.
 DR SMART; SM00600; FN3_2.
 DR PROSITE; PS01166; EGF_2; 1.
 DR PROSITE; PSS0863; FN3_2; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 KM RECEPTOR.
 SQ SEQUENCE 610 AA; 68285 MW; E61310A72FE1E739 CRC64;

Query Match 99.9%; Score 3239; DB 2; Length 610;
 Best Local Similarity 99.8%; Pred. No. 1,le-234;
 Matches 609; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTQTRPSPWIIICYYIWLGFARHGEAQAKEVLLDLSKAQQTLEWISSPPSGMEIRISG 60
 DB 1 MVTQTRPSPWIIICYYIWLGFARHGEAQAKEVLLDLSKAQQTLEWISSPPSGMEIRISG 60
 QY 61 LDENVTPRIITYOVQVMEPNOMNLRTNWSKGAQRI FVELKFTLDPKNSLPGLVATGCK 120
 DB 61 LDENVTPRIITYOVQVMEPNOMNLRTNWSKGAQRI FVELKFTLDPKNSLPGLVATGCK 120
 QY 121 ETPFLYYEEDYDGRNIRENLYKIDITIADESFOTGDDGERMKKANTVREIIGPSISK 180
 DB 121 ETPFLYYEEDYDGRNIRENLYKIDITIADESFOTGDDGERMKKANTVREIIGPSISK 180
 QY 181 GFYLAFFODVAGCIALVSVKYYKKCWITIVENLAVFPTVGSSESSSLVVRGTCVSSAAE 240
 DB 181 GFYLAFFODVAGCIALVSVKYYKKCWITIVENLAVFPTVGSSESSSLVVRGTCVSSAAE 240
 QY 241 EAENSPPMWSAEGEWLVPIGKCI CKAGYQOGKPTCEPCGRFRFYKSSSOTLQSCRPTHS 300
 DB 241 EAENSPPMWSAEGEWLVPIGKCI CKAGYQOGKPTCEPCGRFRFYKSSSOTLQSCRPTHS 300
 QY 301 FSDREGSSRCEGEGYRAASDPYVACTRPPSAPOULININOTYSLFWSPPADNGR 360
 DB 301 FSDREGSSRCEGEGYRAASDPYVACTRPPSAPOULININOTYSLFWSPPADNGR 360

DB 301 FSDREGSSRCEGEGYRAASDPYVACTRPPSAPOULININOTYSLFWSPPADNGR 360
 QY 361 NDVTYRLCKRCGMEQECVPCGSGNIGYMPQOGLGENDYVMDLAAHANYTEFEAVNG 420
 DB 361 NDVTYRLCKRCGMEQECVPCGSGNIGYMPQOGLGENDYVMDLAAHANYTEFEAVNG 420
 QY 421 VSDLSRSQRLFAVSIITGQAPDSQVSGVKKERVLQSRVQLSQOEPHPNGVITEYEIKY 480
 DB 421 VSDLSRSQRLFAVSIITGQAPDSQVSGVKKERVLQSRVQLSQOEPHPNGVITEYEIKY 480
 QY 481 YENDQERRTSTLKTSTASINNLKPGTYVROIAVTAAGYGNVSPRLDVATLEBASG 540
 DB 481 YENDQERRTSTLKTSTASINNLKPGTYVROIAVTAAGYGNVSPRLDVATLEBASG 540
 QY 541 KMEFATVSSQNPVLIIVAVAGTIIIVFWFGFIIIGRHGCGSKADQGEDELYFHS 600
 DB 541 KMEFATVSSQNPVLIIVAVAGTIIIVFWFGFIIIGRHGCGSKADQGEDELYFHS 600
 QY 601 LVTNEHLVSL 610
 DB 601 LVTNEHLVSL 610

RESULT 2
 EPA7_MOUSE STANDARD; PRT; 998 AA.
 AC 061772; 061505; 061773; 061774;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (tyrosine-protein
 DE kinase) (EBK) (Developmental kinase-3) (Embryonic brain
 DE kinase) (EBK) (Synonyms=Edk, Ehk3, Mdk1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=95124729; PubMed=7824284;
 RA Ciosek T., Millauer B., Ulrich A.;
 RT "Identification of alternatively spliced mRNAs encoding variants of
 RT Mdk1, a novel receptor tyrosine kinase expressed in the murine nervous
 RT system";
 RL Oncogene 10:97-108(1995).
 RN [2]
 RP SEQUENCE OF 431-998 FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=96081374; PubMed=8541219; DOI=10.1016/0925-4773(95)00411-S;
 RA Ellis J., Liu Q., Breiten M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Tempest H.V., Warren S., Milr E., Schilling H.,
 RA Fletcher F.A., Ziegler S.F., Rogers J.H.;
 RT "Embryo brain kinase: a novel gene of the eph/ek receptor tyrosine
 RT kinase family";
 RL Mech. Dev. 52:319-341(1995).
 RN [3]
 RP INTERACTIONS WITH PRKCAP AND GRIP1.
 RX MEDLINE=9908206; PubMed=8883737; DOI=10.1016/S0896-6273(00)80663-7;
 RA Torres R., Firestein B.L., Dong H., Staudinger J., Olson E.N.,
 RA Huganir R.L., Bredt D.S., Gale N.W., Yancopoulos G.D.;
 RT "PDZ proteins bind, cluster, and synaptically colocalize with Eph
 RT receptors and their ephrin ligands";
 RL Neuron 21:1453-1463(1998).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with PRKCAP and GRIP1.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;

CC	Name=1; Synonyms=MDK1;
CC	Isoid=061772-1; Sequence=Displayed;
CC	Name=2; Synonyms=MDK1-1;
CC	Isoid=061772-2; Sequence=VSP_003006;
CC	Name=3; Synonyms=MDK1-2;
CC	Isoid=061772-3; Sequence=VSP_003007;
CC	Name=4; Synonyms=MDK1-TL;
CC	Isoid=061772-4; Sequence=VSP_003008, VSP_003009;
CC	Name=5; Synonyms=MDK1-T2;
CC	Isoid=061772-5; Sequence=VSP_003010, VSP_003011;
CC	- TISSUE SPECIFICITY: Widely expressed in embryo. In adult,
CC	expression restricted to hippocampus, testis and spleen.
CC	- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC	receptor subfamily.
CC	- SIMILARITY: Contains 2 fibronectin type III domains.
CC	- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC	-----
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-slb.ch/announce/)
CC	or send an email to license@ibb-slb.ch).
CC	-----
DR	EMBL; X79082; CAA55687.1; -;
DR	EMBL; X79083; CAA55688.1; -;
DR	EMBL; X79084; CAA55689.1; -;
DR	EMBL; X81466; CAA57224.1; -;
DR	PIR; I48612; I48612.
DR	PIR; I48614; I48614.
DR	PIR; JC5672; JC5672.
DR	HSSP; P54763; IJPA.
DR	MGI; MGI:95276; Epha7.
DR	Interpro; IPRO06209; EGF_lke.
DR	Interpro; IPRO01090; Ephrin_receptor.
DR	Interpro; IPRO03961; FN_III.
DR	Interpro; IPRO08957; FN_III-like.
DR	Interpro; IPRO03962; FNIII_subd.
DR	Interpro; IPRO08979; Gal bind_lke.
DR	Interpro; IPRO09030; Grow fac recept.
DR	Interpro; IPRO11009; Kinase_lke.
DR	Interpro; IPRO00719; Prot_Kinase.
DR	Interpro; IPRO01660; SAM.
DR	Interpro; IPRO01245; TYR_pkinase.
DR	Interpro; IPRO08266; TYR_pkinase_AS.
DR	Interpro; IPRO01426; Ykase_receptorV.
DR	Pfam; PF01404; Ephrin_Ibd; 1.
DR	Pfam; PF00041; fn3; 2.
DR	Pfam; PF00069; Pkinase; 1.
DR	Pfam; PF00536; SAM; 1.
DR	PRINTS; PR00014; FNTYPEITII.
DR	PRINTS; PR00109; FTKINASE.
DR	ProDom; PD001495; Ephrin_receptor; 1.
DR	ProDom; PD000001; Prot_kinase; 1.
DR	SMART; SMO0615; EPH_Ibd; 1.
DR	SMART; SMO0060; FN3_2.
DR	SMART; SMO0454; SAM; 1.
DR	SMART; SMO0219; Tykc; 1.
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR	PROSITE; PS50853; FN3; 2.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR	PROSITE; PS50105; SAM_DOMAIN; 1.
KW	Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
KW	Receptor; Repeat; Signal; Transferase; Transmembrane;
KW	Tyrosine-protein kinase.
FT	SIGNAL 1 29 Potential.
FT	CHAIN 30 998 Ephrin type-A receptor 7.
FT	DOMAIN 30 556 Extracellular (Potential).

[illegible]

Db 421 VSDLSRSQRLFAVAVSTTGOAPASQVSGWVKERVLSQVLSWQEPHNGVITEYIKY 480
Qy 481 YEKDQERTYSTLTKTSTASINNLKPGTYVYFQIRAVTAAGYNSPRLLVATLEBASG 540
Db 481 YEKDQERTYSTLTKTSTASINNLKPGTYVYFQIRAVTAAGYNSPRLLVATLEBASG 540
Qy 541 KMEFATVSSQNPVILIAVAVAGTIIIVFMVFGFIIGRHCGYSQADQGEDELYFH 599
Db 541 KMEFATVSSQNPVILIAVAVAGTIIIVFMVFGFIIGRHCGYSQADQGEDELYFH 599
RESULT 3
Q8R381 PRELIMINARY; PRT; 994 AA.
ID Q8R381
AC Q8R381
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epha7 protein.
GN Name=Epha7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2EHC II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derse J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hale F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Abramson R.D., Mullan S.J.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Besek S.A., McEwan P.J., McKernan K.J., Malek J.A., Guneratne P.H.,
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltón E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnski M.I., Skalska U., Smalins D.E., Scherch A., Schain J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C2EHC II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.
DR EMBL: BC026153; AAH26153.1; -.
DR HSP: P54763.1; UPA.
DR MGD: MGI:95276; Epha7.
DR GO: GO:0005615; C:intracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR01090; Ephrin receptor.
DR InterPro: IPR003962; FcIII subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR008979; Gal_bind_like.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR01009; Kinase like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR001660; SAM.

DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR InterPro: IPR001426; Tykase_receptor_V.
DR Pfam: PF01404; Ephrin_1bd; 1.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00536; SAM_1.1.
DR PRINTS: PR00014; ENTPEIIT.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD001495; Ephrin_receptor; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00615; Eph_1bd; 1.
DR SMART: SM00060; FN3_2.
DR SMART: SM00454; SAM; 1.
DR SMART: SM00219; TykC; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS50853; FN3_2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PS50105; SAM_DOMAIN; 1.
DR ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transferase; Transmembrane; Tyrosine-protein kinase
SQ SEQUENCE 994 AA; 111386 MW; A28F98BD964F2EB8 CRC64;
Query Match 98.3%; Score 3188; DB 2; Length 994;
Best Local Similarity 99.3%; Pred. No. 1.5e-230;
Matches 599; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MVQTPSPSIIICITWLGFAHTGAQAKEYLLDLSAQOQTELEWISSPPSGWEISG 60
Db 1 MVQTFPPSIIICITWLGFAHTGAQAKEYLLDLSAQOQTELEWISSPPSGWEISG 60
Qy 1DENYPIRTIYQVCQWEPNQNMMRTNWSKNAORIFVELKFTLRDNCSLPGVIGTCK 120
Db 1DENYPIRTIYQVCQWEPNQNMMRTNWSKNAORIFVELKFTLRDNCSLPGVIGTCK 120
Qy 121 EFNFLVYETDVTGGRNIRENLYVKIDTIADESFTQDGLGERMKLNTREIGPLSKK 180
Db 121 EFNFLVYETDVTGGRNIRENLYVKIDTIADESFTQDGLGERMKLNTREIGPLSKK 180
Qy 181 GFLLAQDVQACIALYSVYVYKKWTIYENLAVFPDVTGSSFLVEVRCVSSAE 240
Db 181 GFLLAQDVQACIALYSVYVYKKWTIYENLAVFPDVTGSSFLVEVRCVSSAE 240
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Db 241 EAENSFRMCSAEGEWLVPIGKICIKAGYQOKGDTCEPCGRFYKSSODLOCSRCPTHS 300
Qy 301 FSDREGSSRCCECDGYRAPSDPYVACTRPPSAPONTLEPQTTVSLSEWSPADNGR 360
Db 301 FSDREGSSRCCECDGYRAPSDPYVACTRPPSAPONTLEPQTTVSLSEWSPADNGR 360
Qy 361 NDVTYIILCKRCGWEQECVPCGSMATGYMPOQGLEDDNYVTWDLAANVTFEVAUNG 420
Db 361 NDVTYIILCKRCGWEQECVPCGSMATGYMPOQGLEDDNYVTWDLAANVTFEVAUNG 420
Qy 421 VSDLSRSQRLFAVAVSTTGOAPASQVSGWVKERVLSQVLSWQEPHNGVITEYIKY 480
Db 421 VSDLSRSQRLFAVAVSTTGOAPASQVSGWVKERVLSQVLSWQEPHNGVITEYIKY 480
Qy 481 YEKDQERTYSTLTKTSTASINNLKPGTYVYFQIRAVTAAGYNSPRLLVATLEBASG 540
Db 481 YEKDQERTYSTLTKTSTASINNLKPGTYVYFQIRAVTAAGYNSPRLLVATLEBASG 540
Qy 541 KMEFATVSSQNPVILIAVAVAGTIIIVFMVFGFIIGRHCGYSQADQGEDELYFH 600
Db 541 KMEFATVSSQNPVILIAVAVAGTIIIVFMVFGFIIGRHCGYSQADQGEDELYFH 600
Qy 601 LVT 603
Db 601 TKT 603

RESULT 4
Q8BSUS PRELIMINARY; PRT: 998 AA.
AC Q8BSUS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length
DE enriched library, clone:5330417H08 product:Eph receptor A7, full
DE insert sequence.
GN Name=Spha7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=C57BL/6J; TISSUE=pituitary gland;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RT Meth. Enzymol. 303:19-44(1999).
RL Nature 409:685-690(2001).
RN [3]
RP STRAIN=C57BL/6J; TISSUE=pituitary gland;
RC MEDLINE=11085660; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RN [4]
RP STRAIN=C57BL/6J; TISSUE=pituitary gland;
RC MEDLINE=204939374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Ozaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP STRAIN=C57BL/6J; TISSUE=pituitary gland;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
RA Ozaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP STRAIN=C57BL/6J; TISSUE=pituitary gland;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
RA Ozaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.
DR EMBL: AK030460; BAC26982.1; -.
DR HSSP: P54763; ITPA.
DR MGJ: MGJ:95276; Epha7.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR InterPro: IPR006209; EGF_lke.
DR InterPro: IPR001090; Ephrin_receptor.
DR InterPro: IPR003962; Fcrl1_subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR008979; Gal_bind_lke.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR011009; kinase_lke.
DR InterPro: IPR007019; Prot_kinase.
DR InterPro: IPR001245; SAM.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR InterPro: IPR001426; Ykase_receptorV.
DR Pfam: PF01404; Ephrin_lbd.1.
DR Pfam: PF00041; En3.1.
DR Pfam: PF00536; SAM_1; 1.
DR PRINTS: PR00104; FNTYPEIIT.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD001495; Ephrin_receptor.1.
DR ProDom: PD000001; Prot_kinase.1.
DR SMART: SM00615; Eph_lbd.1.
DR SMART: SM00060; FN3.2.
DR SMART: SM00454; SAM.1.
DR SMART: SM00219; TYRKC.1.
DR PROSITE: PS001166; EGF_2.1.
DR PROSITE: PS50853; FN3.2.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V.1.1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V.2.1.
DR PROSITE: PS50105; SAM_DOMAIN.1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transferrase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 998 AA; 11859 MW; FCA1E83490E746E1 CRC64;
Query Match 98.3%; Score 3187; DB 2; Length 998;
Best Local Similarity 99.8%; Pred. No. 1.8e-230;
Matches 598; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVVQTRPSPWIIICYLWLGFAHTGEQAQAEVLLDLSKAQOTELEWISSPPSGMERISG 60
Db 1 MVVQTRPSPWIIICYLWLGFAHTGEQAQAEVLLDLSKAQOTELEWISSPPSGMERISG 60
QY 61 LDENVYPIRTYQVCQWEPNQNMMRLTNWISKNAQRIPELKFLLDNCNSLPVIGCTCK 120
Db 61 LDENVYPIRTYQVCQWEPNQNMMRLTNWISKNAQRIPELKFLLDNCNSLPVIGCTCK 120
QY 121 EFTNLVYFEDYDYGRIENLTVKIDITLADSSFTQGDIGERMKNTVREIGPLSKK 180
Db 121 EFTNLVYFEDYDYGRIENLTVKIDITLADSSFTQGDIGERMKNTVREIGPLSKK 180
QY 181 GFYLAPODVACIALSVKYYKKCWITVENLAVPDTVTGSEFSSLVEVGTGVSSAAE 240
Db 181 GFYLAPODVACIALSVKYYKKCWITVENLAVPDTVTGSEFSSLVEVGTGVSSAAE 240
QY 241 EAENSPRMHCSAAGEWLVPIGKICIKAGYQOKGDTCEPCGRPRFYKSSSQDLCRCPTHS 300
Db 241 EAENSPRMHCSAAGEWLVPIGKICIKAGYQOKGDTCEPCGRPRFYKSSSQDLCRCPTHS 300

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QY 301 FSDREGSSRCECDGYRAESDPPEYVACTRPPSAPQNLININQTVLSLEWSPADNGR 360
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QY 361 NDVTYRLCRGCGMEQCEPCPGSNIGYMPQQTGLENTYTWDLAHAYTEFEVAVNG 420
Db 361 NDVTYRLCRGCGMEQCEPCPGSNIGYMPQQTGLENTYTWDLAHAYTEFEVAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGGAAPSOVSGWAKERVLQSVLSMOEPHPGVITEYIKY 480
Db 421 VSDLSRSQRLFAAVSITTTGGAAPSOVSGWAKERVLQSVLSMOEPHPGVITEYIKY 480
QY 481 YEKDQRRRTYSTLTKTSTASINNLKPGTVYFQIRAVTAGYGNVSPRIDVATLEBASG 540
Db 481 YEKDQRRRTYSTLTKTSTASINNLKPGTVYFQIRAVTAGYGNVSPRIDVATLEBASG 540
QY 541 KMEFATVASEQNPVITIAVAVAGTIIIVMVFGLIGRRHCGYSADDEGEBELYFH 599
Db 541 KMEFATVASEQNPVITIAVAVAGTIIIVMVFGLIGRRHCGYSADDEGEBELYFH 599

RESULT 5
EPAT_RAT STANDARD; PRT; 998 AA.
ID EPAT7 RAT
AC P54759;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor EHK-3) (Eph homolog kinase-3).
GN Name=Epha7; Synonyms=Ehk-3, Ehk3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RX MEDLINE=95249272; Pubmed=7731712;
RA Valenzuela D.M., Rojas E., Griffiths J.A., Compton D.L., Gisser M.,
RA Ip N.Y., Goldfarb M., Yancopoulos G.D.;
RT "Identification of full-length and truncated forms of EHK-3, a novel
RT member of the Eph receptor tyrosine kinase family."
RL Oncogene 10:1573-1580(1995).
CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC ephrin-A1, -A2, -A3, -A4 and -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Interacts with PRKCAP and GRIP1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P54759-1; Sequence=Displayed;
CC Note=More widely expressed in the embryo;
CC Name=Short;
CC IsoId=P54759-2; Sequence=VSP_003012;
CC -1- Note=Lacks the kinase domain;
CC -1- TISSUE SPECIFICITY: Restricted to the nervous system.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC receptor subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U21954; AAA86830.1; -.

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DR EMBL; U21955; AAA86831.1; -.
DR HSSP; P54763; IJPA.
DR RGD; 70957; Epha7.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR003964; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR008979; Gal_bind like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR01660; SAM.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR001426; YKase_receptorV.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PR00041; fn3_2.
DR Pfam; PR00669; Kinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; ENTPEIIL.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PSS0853; FN3_2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PSS0105; SAM_DOMAIN; 1.
DR KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
DR Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 24
FT CHAIN 25 998
FT DOMAIN 25 556
FT TRANSMEM 557 577
FT DOMAIN 578 998
FT DOMAIN 192 328
FT DOMAIN 331 433
FT DOMAIN 443 535
FT DOMAIN 633 894
FT DOMAIN 923 987
FT SITE 996 998
FT NP_BIND 639 647
FT BINDING 665 665
FT ACT_SITE 758 758
FT MOD_RES 608 608
FT MOD_RES 614 614
FT MOD_RES 791 791
FT MOD_RES 940 940
FT CARBOHYD 343 343
FT CARBOHYD 410 410
FT VARSPIC 600 610
FT SEQUENCE 998 AA; 111953 MW; A7A82A698924876C CRC64;
SQ
Query Match 97.9%; Score 3175; DB 1; Length 998;
Best Local Similarity 99.2%; Pred. No. 1,4e-229;
Matches 594; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 MVQTRPPSWITLCYIWLGFHTGSAQAKEYLLDSRAQOTLEWISSPPSGWEISG 60

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Db 1 MVTQTRYSWILLIYIMLGFAHGEAAAEVLLLSKAQOTLEWISSPSSGWEETISG 60
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Db 61 LDEVTPIRTYQVQCVNPNQNNMLRTWISKGNAGNORFVELKPLRDQNSLPGLGTCK 120
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Qy 181 GFYIAPQDVACIALVSVKYYKCKWTIVENLAFPPDTVTSSPSLSLVEFGTCYSSAE 240
Db 181 GFYIAPQDVACIALVSVKYYKCKWTSIENLAFPPDTVTSSPSLSLVEFGTCYSSAE 240
Qy 241 EAENSPPHNGSAEEMLVPIGKCI CKAGYQKQKGPCEPCGRFPKSSGODIQSCRPHS 300
Db 241 EAENSPPHNGSAEEMLVPIGKCI CKAGYQKQKGPCEPCGRFPKSSGODIQSCRPHS 300
Qy 301 FSDREGSSRCEDEGYRAPSDPPYVACTRPPSAPOULIFNINOTTVSLEWSPPADNGR 360
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Qy 361 NDVTYRILCKRCSEWQECVPCGSGNIGMPQOTGLEEDNYTVMDLLAHANTFEVEAVNG 420
Db 361 NDVTYRILCKRCSEWQECVPCGSGNIGMPQOTGLEEDNYTVMDLLAHANTFEVEAVNG 420
Qy 421 VSDLSRSORLEAASVITTGGAAPQSVGMVERLQSVLSWQEPHEPNVITEYEYKY 480
Db 421 VSDLSRSORLEAASVITTGGAAPQSVGMVERLQSVLSWQEPHEPNVITEYEYKY 480
Qy 481 YEKQQRERTYTLTKSTASINNLKPGTVVFOIRAVTAAGYNSPRLDVATLEBASG 540
Db 481 YEKQQRERTYTLTKSTASINNLKPGTVVFOIRAVTAAGYNSPRLDVATLEBASG 540
Qy 541 KMFPAIVSSQNPVITIAVAVAGTILVMTFGFIIGRRHCGYSKADQSGDELYFH 599
Db 541 KMFPAIVSSQNPVITIAVAVAGTILVMTFGFIIGRRHCGYSKADQSGDELYFH 599

RESULT 6
EPAT_HUMAN STANDARD; PRT; 998 AA.
ID Q15375; Q9H124;
AC 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor EHK-3) (Eph homology kinase-3) (Receptor protein-
DE tyrosine kinase HEK11).
GN Name=EPHA7; Synonyms=EHK3, HEK11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95206782; PubMed=7898931;
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA Baas R., Welcher A.A.;
RT "cDNA cloning and tissue distribution of five human Eph-like receptor
RT protein-tyrosine kinases";
RL Oncogene 10:897-905(1995).
RN [2]
RP SEQUENCE OF 1-277 FROM N.A.
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC ephrin-A1, -A2, -A3, -A4 and -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Interacts with PRKCBP and GRIP1 (By similarity).
```

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CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC receptor subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).

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FT MOD_RES 614 614 Phosphotyrosine (by autocalysis)
FT (Potential)
FT MOD_RES 791 791 Phosphotyrosine (by autocalysis)
FT (Potential)
FT MOD_RES 940 940 Phosphotyrosine (by autocalysis)
FT (Potential)
FT CARBOHYD 343 343 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 410 410 N-linked (GlcNAc...) (Potential)
SQ SEQUENCE 998 AA; 112096 MW; 479B9CA0D2BB06EB CRC64;

Query Match 96.8%; Score 3139; DB 1; Length 998;
Best Local Similarity 97.7%; Pred. No. 7.3e-227;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVTQTRFPSPWIIICYLWLGFAHTGSAQAKEYLLDLSKAQTELEWISSPSPGWERISG 60
DB 1 MVTQTRFPSPWIIICYLWLGFAHTGSAQAKEYLLDLSKAQTELEWISSPSPGWERISG 60
QY 61 LBNYTPIRITYQVCQWEPNQNWLRTNWSKNAQRIFVELKFTLDCNSLPGVLGTC 120
DB 61 LBNYTPIRITYQVCQWEPNQNWLRTNWSKNAQRIFVELKFTLDCNSLPGVLGTC 120
QY 121 ETENLYYEEDYDYGRIENLYVKIDTIADESFTQGDIGERRKMLNTEVREIGPLSK 180
DB 121 ETENLYYEEDYDYGRIENLYVKIDTIADESFTQGDIGERRKMLNTEVREIGPLSK 180
QY 181 GFYLAPODVACIALYSVKYYKKCWITVENLAVFPDTVGSEFSSLVEVRGTCVSSAAE 240
DB 181 GFYLAPODVACIALYSVKYYKKCWITVENLAVFPDTVGSEFSSLVEVRGTCVSSAAE 240
QY 241 EAENSPPRMHCSAGEWLVPIGKICAKAGYQOKDTCPCRRRYKSSQQLQCSRCTHS 300
DB 241 EAENSPPRMHCSAGEWLVPIGKICAKAGYQOKDTCPCRRRYKSSQQLQCSRCTHS 300
QY 241 EAENAPPMHCSAGEWLVPIGKICAKAGYQOKDTCPCRRRYKSSQQLQCSRCTHS 300
DB 301 FSPREGSSRECEGDYRAPSDPYVACTPSPAPQLININQTVLSLWSPADNGR 360
QY 301 FSPREGSSRECEGDYRAPSDPYVACTPSPAPQLININQTVLSLWSPADNGR 360
QY 361 NDVTYRLICRCRSGWEGECVPCSGNIGYMQGTGLIEDNYTVMDLAAHYTEVEAVNG 420
DB 361 NDVTYRLICRCRSGWEGECVPCSGNIGYMQGTGLIEDNYTVMDLAAHYTEVEAVNG 420
QY 421 VSDLSRSQRLFAVVSITGQAAPSOVSGWKEKRVLSQEPHPHCATTEYEIKY 480
DB 421 VSDLSRSQRLFAVVSITGQAAPSOVSGWKEKRVLSQEPHPHCATTEYEIKY 480
QY 481 YEKDQRERTSTLKTSTASINNLKRGTYVYVQIRAFATAGYGNVSPRIDVATLEBASG 540
DB 481 YEKDQRERTSTLKTSTASINNLKRGTYVYVQIRAFATAGYGNVSPRIDVATLEBASG 540
QY 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFVFGF-GGRRHCGYSKADCEGDELYFH 599
DB 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFVFGFIIIGRRHCGYSKADCEGDELYFH 599

RESULT 7
Q8C7N2 PRELIMINARY; PRT; 593 AA.
ID Q8C7N2 PRELIMINARY; PRT; 593 AA.
AC Q8C7N2;
DT 01-MAR-2003 (Tremblere) 23, Created)
DT 01-MAR-2003 (Tremblere) 23, Last sequence update)
DT 01-MAR-2004 (Tremblere) 26, Last annotation update)
DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
DE library, clone: C6300306 product: Eph receptor A7, full insert
DE sequence.
GN Name=EphA7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;

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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Taahiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK049848; BAC33955.1; -.
DR HSSP; P54763; INUK.
DR MKD; MGI:95276; EphA7.
DR GO; GO:0005615; Extracellular space; TAS.
DR GO; GO:0016021; C:Integral to membrane; TAS.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR003962; Ephrin subd.
DR InterPro; IPR003961; FN-III.
DR InterPro; IPR008957; FN-III-like.
DR InterPro; IPR008979; Gal_bind-like.
DR InterPro; IPR001426; YKase receptorV.
DR Pfam; PF01404; Ephrin_1bd_1.
DR Pfam; PF00041; fn3_1.
DR PRINTS; PR00014; EPHRYEIII.
DR ProDom; PD001495; Ephrin_receptor; 1.

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DR SMART; SM00615; Eph_1bd; 1.
 DR SMART; SM00600; FN3; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 KW RECEPTOR.
 SQ SEQUENCE. 593 AA; 66324 MW; 11980225D73F3D83 CRC64;
 Query Match 96.4%; Score 3126; DB 2; Length 593;
 Best Local Similarity 99.7%; Pred. No. 3.3e-226;
 Matches 587; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVVQTRPSPWIIICYLWLGFAHTGEAQAQAEVLLDLSKAQOTLEWISSPPSGMEETISG 60
 DB 1 MVVQTRPSPWIIICYLWLGFAHTGEAQAQAEVLLDLSKAQOTLEWISSPPSGMEETISG 60
 QY 61 LDENVTPRTYQVQVQVMEPNQNNMLRTNWSKGNARIFVELKTTLRDQNSLPVGLGTC 120
 DB 61 LDENVTPRTYQVQVQVMEPNQNNMLRTNWSKGNARIFVELKTTLRDQNSLPVGLGTC 120
 QY 121 ETEFLYYETDYDGRNIRENLYVKIDTIADESFTQDGERGKXKTEVREIGPLSKK 180
 DB 121 ETEFLYYETDYDGRNIRENLYVKIDTIADESFTQDGERGKXKTEVREIGPLSKK 180
 QY 181 GFYLAPODVGACIALVSKVYKKCWITVENIAVFPPVTGSEFSSSLVEVAGTCVSSAEE 240
 DB 181 GFYLAPODVGACIALVSKVYKKCWITVENIAVFPPVTGSEFSSSLVEVAGTCVSSAEE 240
 QY 241 EAENSPPMHCSAGEEMLVPIGKCIQAGYQKGDTCBPCGRFYKSSQDLQCSRCPHTS 300
 DB 241 EAENSPPMHCSAGEEMLVPIGKCIQAGYQKGDTCBPCGRFYKSSQDLQCSRCPHTS 300
 QY 301 FSDREGSSRCCEGGRAPSDPYVACTRPSPAPQNLIFINQTVLSLESPADNGR 360
 DB 301 FSDREGSSRCCEGGRAPSDPYVACTRPSPAPQNLIFINQTVLSLESPADNGR 360
 QY 361 NDVTYRILCKRCSEGECEVPCGSNIGMPQOTGLENNYVVMLLAHANTFEVAVNG 420
 DB 361 NDVTYRILCKRCSEGECEVPCGSNIGMPQOTGLENNYVVMLLAHANTFEVAVNG 420
 QY 421 VSDISRSQRLFAVSIITGQAAPQSVGVMKERVLOSQVQSWQEPHPNGVITEYIKY 480
 DB 421 VSDISRSQRLFAVSIITGQAAPQSVGVMKERVLOSQVQSWQEPHPNGVITEYIKY 480
 QY 481 YENDQRRRTYSTLKSTSTASINNLKPGTYVFPQIRYTAAGYGNVSPRLDVALTEASG 540
 DB 481 YENDQRRRTYSTLKSTSTASINNLKPGTYVFPQIRYTAAGYGNVSPRLDVALTEASG 540
 QY 541 KMFPEATVSSSEONVITIAVAVAGTIIIVPMVGFIIIRRHGYSRAD 589
 DB 541 KMFPEATVSSSEONVITIAVAVAGTIIIVPMVGFIIIRRHGYSRAD 589

RESULT 8
 EPAR7 CHICK STANDARD; PRT; 993 AA.
 ID AC 062423;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor CEPHA7) (Tyrosine-protein kinase receptor CEK11).
 GN Name=EPHA7; Synonyms=CEK11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 OC NCBI_TaxID=9031;
 RX RN 1;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 MDLLINE=98092111; PubMed=9431814; DOI=10.1016/S0925-4773(97)00147-0;

RA Araujo M., Nieto M.A.;
 RT "The expression of chick EphA7 during segmentation of the central and peripheral nervous system";
 RL Mech. Dev. 68:173-177(1997).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Within the nervous system, expression is restricted to prosomeres 1 and 2 in the diencephalon and all the rhombomeres in the hindbrain during segmentation stages. Later on, a superimposed pattern appears that correlates with the formation of several axonal tracts. In the somitic mesoderm, the expression correlates with segmentation and the guidance of both neural crest and motor axons through the sclerotomes.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
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 CC -----
 CC EMBL; Y14271; CAA74643.1; -.
 DR HSBP; P54763; IJPA.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin receptor.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003962; FNIII subd.
 DR InterPro: IPR008979; Gal bind like.
 DR InterPro: IPR009030; Grow fac recept.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001660; SAM.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase AS.
 DR InterPro: IPR001426; YKase receptorV.
 DR Pfam; PF01404; Ephrin_1bd; 1.
 DR Pfam; PF00041; FN3_2.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR001014; FNTYPEIIT.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD0001495; Ephrin_receptor; 1.
 DR ProDom; PD0000001; Prot_kinase; 1.
 DR SMART; SM00615; Eph_1bd; 1.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TYRK; 1.
 DR SMART; SM00186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00853; FN3_2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS00105; SAM_DOMAIN; 1.
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 30
 FT CHAIN 31 993
 FT DOMAIN 31 551
 FT TRANSMEM 552 572
 FT DOMAIN 573 993
 FT DOMAIN 192 328
 FT DOMAIN 331 433
 FT DOMAIN 443 535
 FT DOMAIN

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FT DOMAIN 628 889 Protein kinase.
FT 918 982 SAM.
FT SITE 991 992 PDZ-binding motif (Potential).
FT NP_BIND 634 642 ATP (By similarity).
FT DISUPID 74 109 By similarity.
FT BINDING 660 660 ATP (By similarity).
FT ACT_SITE 753 753 By similarity.
FT MOD_RES 603 603 phosphotyrosine (by autocatalysis)
FT MOD_RES 609 609 phosphotyrosine (by autocatalysis)
FT MOD_RES 786 786 phosphotyrosine (by autocatalysis)
FT MOD_RES 935 935 phosphotyrosine (by autocatalysis)
FT CARBOHYD 343 343 N-linked (GlcNAc...) (Potential).
FT FT 410 410 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 993 AA; 111366 MW; EECF9603047606BD CRC64;

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Query Match 93.5%; Score 3031.5; DB 1; Length 993;
Best Local Similarity 94.5%; Pred. No. 8,7e-219;
Matches 566; Conservative 17; Mismatches 11; Indels 5; Gaps 1;

```

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QY 1 MVTQTPSPSWIIICLYTWLGPHTGEAQAKEYLLDLSKAQOTLEWISSPPSGMEISG 60
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1 MVLRSRLPWPIMLCVWLIRFAHTGEAQAKEYLLDLSKAQOTLEWISSPPSGMEISG 60
QY 61 LDENYPIRIRYQCVQWNEPNNMLRTNWTISKGAORIPEWELKPTLBDCKSLPGVLTGCK 120
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 61 LDENYPIRIRYQCVQWNEPNNMLRTNWTISKGAORIPEWELKPTLBDCKSLPGVLTGCK 120
QY 121 EFTNLVYETDYDTGRNIRENLVYKIDITIADESFTOGDGERMKLNTVREIGPLSKK 180
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 121 EFTNLVYETDYDTGRNIRENLVYKIDITIADESFTOGDGERMKLNTVREIGPLSKK 180
QY 121 EFTNLVYETDYDTGRNIRENLVYKIDITIADESFTOGDGERMKLNTVREIGPLSKK 180
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 121 EFTNLVYETDYDTGRNIRENLVYKIDITIADESFTOGDGERMKLNTVREIGPLSKK 180
QY 181 GFYIAFDVACIALVSVKYYKKCMITVENLAFPTVTGSEPSLSVEKRGTCVSSAEE 240
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 181 GFYIAFDVACIALVSVKYYKKCMITVENLAFPTVTGSEPSLSVEKRGTCVSSAEE 240
QY 241 EAENSPPMHCSAEGEMLVPIGKICRKGYOQKGTCPGCRFRFXSSSOLQSCRCTHS 300
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 241 EAENSPPMHCSAEGEMLVPIGKICRKGYOQKGTCPGCRFRFXSSSOLQSCRCTHS 300
QY 301 FSDREGSSRCEDBGYRAPSDPPYVACTPPSPAPQMLFINIQTVTLEWSPPADNGR 360
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 301 FSDREGSSRCEDBGYRAPSDPPYVACTPPSPAPQMLFINIQTVTLEWSPPADNGR 360
QY 361 NDVTYRILCRCSWEGECVPCGSNIGMPQOTGLENNYTTWMDLAAHAYTEFEAVNG 420
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 361 NDVTYRILCRCSWEGECVPCGSNIGMPQOTGLENNYTTWMDLAAHAYTEFEAVNG 420
QY 421 VSDLSRQRLPAANSITGGAAPQVSGWKEKRLQSVLDSWEPHPGVITEYIKY 480
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 421 VSDLSRQRLPAANSITGGAAPQVSGWKEKRLQSVLDSWEPHPGVITEYIKY 480
QY 481 YEKDQRERTYTLTKSTASINNLAKPGTVVFOIRATVAGYGVSPRI DVATLEASG 540
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 481 YEKDQRERTYTLTKSTASINNLAKPGTVVFOIRATVAGYGVSPRI DVATLEASG 540
QY 541 KMEFATVSSQNFVITIAVAVAGTITLVPMVFGFIIGRRHCGYKADLEGDELYFH 599
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 540 ----ATAVSSQNFVITIAVAVAGTITLVPMVFGFIIGRRHCGYKADLEGDELYFH 599

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RESULT 9
Q8C276 PRELIMINARY; PRT; 681 AA.
AC Q8C276;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Mus musculus 10 days neonate olfactory brain cDNA, RIKEN full-length
entriched library, clone:E530015D21 product:l Eph receptor A5, full

```

```

DE insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/15055500;
RA Carninci P., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Komno H., Akiyama U., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi T., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multipipillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S.,
RA Kishihara C., Matsuyama T., Miyazaki A., Morita M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089143; BC040764.1; -.
DR HSP; P54763; INUK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005003; F:ephrin receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.

```

DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin_receptor.
 DR InterPro: IPR003962; FcIII subd.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR008979; Gal_bind like.
 DR InterPro: IPR009030; Grow_fac_recept.
 DR InterPro: IPR001426; YKase_receptor.
 DR Pfam: PF00404; Ephrin_lbd_1.
 DR Pfam: PF00041; fn3_2.
 DR PRINTS: PR00014; FNTYPEIII.
 DR ProDom: PD001495; Ephrin_receptor; 1.
 DR SMART: SM00615; EPH_lbd; 1.
 DR SMART: SM00605; FN3_2.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00853; FN3_2; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 KM Receptor.
 SQ SEQUENCE 681 AA; 75336 MW; 92B9187AB78BE722 CRC64;

Query Match 57.4%; Score 1862.5; DB 2; Length 681;
 Best Local Similarity 56.6%; Pred. No. 3.9e-131;
 Matches 351; Conservative 98; Mismatches 136; Indels 35; Gaps 9;

QY RFPSSWILCY-----IM-----LLGFHTEGAQAAKEVLLDLSKAQOQTELEWISSPPSG 54
 DB RVPSSLAGCYSAPLKGPIWTLCLCALRTLLASPSNEVNLDSRTYWGDLGWIAPFGNG 84
 QY WEISIGLDENYTPRTYQVCVMEPNQNNMLRTNWSKGNQRIFFVELKFTLRQNSLPG 114
 DB WEISIGLDENYTPRTYQVCVMEPNQNNMLRTNWSKGNQRIFFVELKFTLRQNSLPG 144
 QY 115 VLGTCKETPNLYYETDYDTRNIRENLYKIDITIADESTQGLGRKKKLTVEYREI 174
 DB 145 GLGTCKETPNLYYETDYDTRNIRENLYKIDITIADESTQGLGRKKKLTVEYADV 204
 QY 175 GPLSKKGFYLAFOVGACIALVSVKVVYKKCMITVENAVPDPVYSEPSLVEVGTG 234
 DB 205 GPLSKKGFYLAFOVGACIALVSVKVVYKKCMITVENAVPDPVYSEPSLVEVGTG 264
 QY 235 VSSAEBAENSPRMCSAEGEMLVPIGKICAGYQOKGDTCEPCGRFRYKSSQDLQCS 294
 DB 265 VN--HSTVDDBPKMHCAGEMLVPIGKCMKACAGEENGTCQYCRPGFFASHSQC 322
 QY 295 RCPHSSPDRSGSRCECEDGYRAPSDPYVACTRPPSPQNLFININQTVSLEWSP 354
 DB 323 KCPHSSYTHEBASISCVCEKDYFRKSDPPPTMACTRPPSPABRNAISNVNETSVLEWTP 382
 QY 355 ADNGGRDVTYRIICKSCSMQEGECVPCGSNIGVMPOQTGEDVYVYMDLAAHNTFE 414
 DB 383 ADTGGRDVTYRIICKSCSMQEGECVPCGSNIGVMPOQTGEDVYVYMDLAAHNTFE 442
 QY 415 VEAANGVSDLSRQSLFAAVSITTGQAAPSOVSGVMEKERVQSRVQSLSMQEPHPNGYT 474
 DB 443 IEAANGVSDLSRQSLFAAVSITTGQAAPSOVSGVMEKERVQSRVQSLSMQEPHPNGYT 502
 QY 475 EYEIKYKQDQRETYSTLTYSASINNIKPGTVYFOIRAVTAAGYGVSPRLDVAT 534
 DB 503 EYEIKYKQDQRETYSTLTYSASINNIKPGTVYFOIRAVTAAGYGVSPRLDVAT 558
 QY 535 LEBSAGMFEAT-----AVSSEONPVIIIAVAVAGTIIIVMVGFIIGRHCHGYSKDO 590
 DB 559 -----FETTPVSVASNDOSQPIIAVSVTVGVILLAVMI-GFLISGRRCGYSKQ 609
 QY 591 EGDEE-LYFSLVTNHLSTV 609
 DB 610 DPBEKMHFH-----NGHIKL 625

RESULT 10
 SPAS_RAT STANDARD; PRT; 1005 AA.

AC P54757;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein
 kinase receptor Ephk-1) (EPH homology kinase-1).
 GN Name=EphA5; Synonyms=Ehk-1, Ekl1;
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
 RP STRAIN=Sprague-Dawley; TISSUE=Brain;
 RC MEDLINE=94067777; PubMed=7504232;
 RA Maisondieu P.C., Barrezaeta N.X., Yancopoulos G.D.;
 RT "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine
 RT kinase family with distinctive structures and neuronal expression.";
 RL Oncogene 8:3277-3288(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=95206467; PubMed=7896466; DOI=10.1016/0306-4522(94)90014-0;
 RA Taylor V., Miescher G.C., Pfaff S., Honegger P., Breitschopf H.,
 RA Laessmann H., Steck A.J.;
 RT "Expression and developmental regulation of Ehk-1, a neuronal Elk-like
 RT receptor tyrosine kinase in brain".
 RL Neuroscience 63:163-178(1994).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=6;
 CC Name=1;
 CC IsoId=P54757-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P54757-2; Sequence=VSP_003001;
 CC Name=3;
 CC IsoId=P54757-3; Sequence=VSP_003002;
 CC Name=4;
 CC IsoId=P54757-4; Sequence=VSP_003002, VSP_003003;
 CC Name=5;
 CC IsoId=P54757-5; Sequence=VSP_003001, VSP_003002, VSP_003003;
 CC Name=6;
 CC IsoId=P54757-6; Sequence=VSP_003000, VSP_003002;
 CC -1- TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
 CC system. Predominantly expressed in neurons.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X78689; CA55357.1; -.
 DR PIR: S49015; S49015.
 DR PIR: S51603; S51603.
 DR HSSP: P54763; 1JPA.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin_receptor.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR008979; Gal_bind like.
 DR InterPro: IPR009030; Grow_fac_recept.
 DR InterPro: IPR001426; YKase_receptor.
 DR InterPro: IPR009030; Grow_fac_recept.

DR InterPro: IPR011039; Kinase_like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001650; SAM.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
 DR InterPro: IPR001426; YKase_receptorV.
 DR Pfam: PF01404; Ephrin_1bd; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; Kinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR PRINTS: PR00014; ENTPELII.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD001495; Ephrin_receptor; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00615; EPH_1bd; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS01166; EGF_2; UNKNOWN_1.
 DR PROSITE: PS50853; FN3; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS50105; SAM_DOMAIN; 1.
 KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
 KW Receptor; Repeat; Signal; Transferrase; Transmembrane;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 26
 FT CHAIN 27 1005
 FT DOMAIN 27 575
 FT TRANSMEM 576 596
 FT DOMAIN 597 1005
 FT DOMAIN 222 356
 FT DOMAIN 471 561
 FT DOMAIN 677 938
 FT DOMAIN 967 1005
 FT NP_BIND 683 691
 FT BINDING 709 709
 FT ACT_SITE 802 802
 FT MOD_RES 652 652
 FT MOD_RES 658 658
 FT MOD_RES 835 835
 FT MOD_RES 984 984
 FT CARBOHYD 266 266
 FT CARBOHYD 301 301
 FT CARBOHYD 371 371
 FT CARBOHYD 425 425
 FT CARBOHYD 438 438
 FT CARBOHYD 463 463
 FT CARBOHYD 10 20
 FT VARSPLIC 306 357
 FT VARSPLIC 358 470
 FT VARSPLIC 597 621
 FT CONFLICT 170 170
 FT CONFLICT 566 566

FT CONFLICT 578 578 G -> A (in Ref. 2).
 FT CONFLICT 669 669 G -> A (in Ref. 2).
 FT CONFLICT 708 708 T -> I (in Ref. 2).
 FT CONFLICT 979 979 T -> I (in Ref. 2).
 SQ SEQUENCE 1005 AA; 111007 MW; 1AED24C99693C574 CRC64;
 Query Match 56.2%; Score 1821; DB 1; Length 1005;
 Best Local Similarity 54.6%; Pred. No. 8; 8e-128;
 Matches 350; Conservative 97; Mismatches 138; Indels 56; Gaps 11;
 QY 6 RPSWIIIC-----IW-----LGFATGGEAQAKEYLLLDSSKQOTELEISPPG 54
 DB 25 RVPASLAGCTSAAPLKPELWICLLCAALRTLLASPSENVLLDSRVLAGLGIAPPKG 84
 QY 55 WEISGLDENYTPRTYOVCOVPEPNQNMRLTNMISKNAORI FVELKFTLLDNCSLPG 114
 DB 85 WEIEGVDEYNAPAIHTYYQCKWEGQNMWLLTWSINSNASRI FIELKFTLLDNCSLPG 144
 QY 115 VLGTCKETPLYYEEDYDTGRINENLYKIDTTLADSSFTQGLGERKMKLNTVEYREI 174
 DB 145 GLGTCKETPLMYEESDDEGRNIMKNOYIKIDTTLADSSFTLGLGDRYMKLNTVEYRDV 204
 QY 175 GPLSKGFYLAPODVACIALVSVKYKKCWITVENLAVFPPTVVGSEPSLVEYRGTC 234
 DB 205 GPLSKGFYLAPODVACIALVSVKYKKCVNHLAVFPPTITGADSSQLIEVSGSC 264
 QY 235 VSSAEBAENSPRMHCSAGEWLVPIGKICRAGYQOKDTCBPCGRFRYKSSODLQCS 294
 DB 265 VN--HSVTDDPPRMHCSAGEWLVPIGKCMCKRAGYEBKNGTCQVCRPGFFKAPHSQTCG 322
 QY 295 RCTTHFSDBREGSRECEDEGYRRASDPPIYACTRPSPAPQNLININQTTYSLEWSP 354
 DB 323 KCPHSHYTHEASTSCVCEKDYFRRESDPPIYACTRPSPAPRAVSNVNETSYFLWIP 382
 QY 355 ADNGANDTYRILCKRCGMEGECVPCGSNIGYMPQOTGLIEDNYTMDLAAHYTFE 414
 DB 383 ADTGKGDVSYTLCKCKNSHACVCECGHRYLQOGLKNTSYMADPLAHTYTFE 442
 QY 415 VEAIVGVSDLSRSQRLFAAVSITTGAPAPSOVGVKKEVLRVSQEPHPNGVIT 474
 DB 443 IEAVNVSDLSPETRGYVSNVTNQAAPSPVTVNKKIAKNSISLSQEPDRPGIIL 502
 QY 475 EYIKIYENDQRERTYTLKYSTASINNLKPGTYVYQIARVTAAGVNSPRLDVAT 534
 DB 503 EYIKIYENDQ--ETSYTIILSKETITTAGLKPSAVYVQIARVTAAGVNSPRRPE--- 558
 QY 535 LEEASGKMEFATV--SSEQNPVITIAVAVAGTIIIVEMVGFII-----GRR- 581
 DB 559 -----FETTVFPAASNDQSIPIIGVSYVGVILLAVMI-GFLISGSCCECGGRAS 609
 QY 582 -----HGYSKADQEGDEE-LYFHSIVTNEHLSV 609
 DB 610 SLCAVAHPILIMCGYSKAKQDPEEKKMFH-----NGHKL 646
 RESULT 11
 ID EPAS_HUMAN STANDARD; PRT; 1037 AA.
 AC P54756;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor, 5 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EHK-1) (Eph homology kinase-1) (Receptor protein-tyrosine kinase HEK7).
 DE Name=EphA5; Synonyms=BHK1, HEK7;
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RA Miescher G.C.;
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 25-1037 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95206782; PubMed=7898931;
 RA Fox G.M., Helset P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
 RT "cDNA cloning and tissue distribution of five human EPH-like receptor
 protein-tyrosine kinases";
 RL Oncogene 10:897-905(1995).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: Type I membrane protein.
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=B54756-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=B54756-2; Sequence=VSP_002999;
 CC -1- TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
 CC system.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X95425; CAAG4700.1; -;
 DR EMBL; L36644; AAA74245.1; -;
 DR HSSP; P54763; 1TBA.
 DR Genew; H9NC;389; EPHAS.
 DR MIM; 600004; -;
 DR GO; GO:0016021; C:Integral to membrane; TAS.
 DR GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001090; Ephrin receptor.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003962; FN III subd.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; Ykase_receptor.v.
 DR Pfam; PF01404; Ephrin_1bd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; ENTPEPIL.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD001495; Ephrin_receptor; 1.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_1bd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TYKIC; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS50853; FN3; 2.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00790; RECEPTOR TYR_KIN_V.1; 1.
 DR PROSITE; PS00791; RECEPTOR TYR_KIN_V.2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
 KW Receptor; Repeat; Signal; Transferrase; Transmembrane;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 24
 FT CHAIN 25 1037 Potential.
 FT DOMAIN 25 573 Ephrin type-A receptor 5.
 FT TRANSMEM 574 594 Extracellular (Potential).
 FT DOMAIN 595 1037 Potential.
 FT DOMAIN 220 354 Cytoplasmic (Potential).
 FT DOMAIN 357 459 Cys-rich.
 FT DOMAIN 469 559 Fibronectin type-III 1.
 FT DOMAIN 675 936 Fibronectin type-III 2.
 FT DOMAIN 965 1029 Protein kinase.
 FT SITE 1035 1037 SAM.
 FT NP_BIND 681 689 PDZ-binding motif (Potential).
 FT BINDING 707 707 ATP (By similarity).
 FT ACT_SITE 800 800 By similarity.
 FT MOD_RES 650 650 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 656 656 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 833 833 Phosphotyrosine (by autocatalysis) (Potential).
 FT MOD_RES 982 982 Phosphotyrosine (by autocatalysis) (By similarity).
 FT CARBOHYD 264 264 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 299 299 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 423 423 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 436 436 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 461 461 N-linked (GlcNAc...) (Potential).
 FT VANSPLIC 597 619 SCCEGCGRASSLCAVHPILIW -> R (in isoform 2).
 FT FT
 FT SO SEQUENCE 1037 AA; 114784 MW; FC2C46C959AFB699 CRC64;
 Query Match 56.1%; Score 1819; DB 1; Length 1037;
 Best Local Similarity 55.1%; Pred. No. 1,36-127;
 Matches 348; Conservative 96; Mismatches 134; Indels 52; Gaps 11;
 QY 6 RFPSSW--IICCYTWLGFPAHTGEAQAKEVLLDSKAQOETLEMISSPPSGMEISGLDE 63
 DB 37 RAPLMTCLILC-----AALRTILASPNEVNLDSRTVMGDLGIAPPKGMEIGEVD 91
 QY 64 NYTPIRTYOVCOVWEPNOMNMLRTNWSKGAQRIIFELKFTLLADCNLSRGVLTCKETP 123
 DB 92 NYAPIHITYOVCKWVEQONNMWLLTWSLSNEGASIFLEKFTLLDNCNSLPGLGCTCKETP 151
 QY 124 NLVYETEDYVTVGRNIRENLVYKIDITIADESFTGGDGERMKNTVREISPKSKGFY 183
 DB 152 NMYTFESDDQNGRKIKENQIKIDITIADESFTLIDGDRMKNTVREIVDGPLSKGFY 211
 QY 184 LAFQDVACIALVSVKYYKKCWITVENLAVFPDVTGSEBSLSVBYRGTCVSSAEBAE 243
 DB 212 LAFQDVACIALVSVRYKKCPVVRHLAVFPDITIGADSSQLLEVSGSVN--HSVTD 269
 QY 244 NSPRMGCSAGEWLVPIGKLCIKRAGYQOKGDTGCPGGRPRPKSSQDLQSCRCTHPSD 303
 DB 270 EPPDMHCSAGEWLVPIGKCMCKRAGYEKKGTCCVCPGPFKASPHIQSCGKCPHSHYTH 329
 QY 304 REGSSRCECEGDYGRAPSDPPYVACTPPAPQNLININQTYVLSLWSPADNGGRNDV 363
 DB 330 EEASTSCVCEKDYFRRSDDPTMACTPPSAPRAISNVAVETSVLEMIIPADTGCKDV 389
 QY 364 TYRILCKRGSWEQCEVPCGSNIGYMQOQTGEDNVTYVMDLLAHANYTEVEAVNGVSD 423
 DB 390 SYTIACKCKNSHAGVCECGHAYVILPRQGLKATYSVMVMDLLAHTYTFEIEAVNGVSD 449

Qy	424	LSRSORLTAASITTTGOAAPSGVSGVMKERVLORSVOLSMOEPHENGYTEYEIKYEK	483
Db	450	LSPGARQYVSNVAVTTNNGAAPSPVTVTKKGIKAKNKSLSLSMOEPDRNGIILEYIHFEX	509
Qy	484	DQREFTYSTLTKTSTASINLNKPGTVYFQIRPAVTAAGYGNYSPLDVAITTEASGKMF	543
Db	510	DQ-ETSYTIKSEKTTTTEAGKSPASVYFQIRAPTAAGYGNYSPLDVAITTEASGKMF	557
Qy	544	EAT---AASSEONPVIIIAVAVAGIILLVFWFGIIL-----GRR-----	581
Db	558	ETTPVFAASSDDQSQIPVIAVSVTVG-VILLAAVIGVLLSGSCCECGGRPSLCAVAHPI	616
Qy	582	---HCGYSKADQDEGDEE-LYFHSLVTNHSLV	609
Db	617	LIMRCGYSKAKQDPBEKMHF-----NGIYKL	644
RESULT 12			
QGBRB1	QGBRB1	PRELIMINARY;	PRT; 984 AA.
ID	01-MAR-2003	(TREKBLrel. 23, Created)	
AC	01-MAR-2003	(TREKBLrel. 23, Last sequence update)	
DT	01-MAR-2004	(TREKBLrel. 26, Last annotation update)	
DE	Mus musculus 9.5 days embryo parthenogenesis cDNA, RIKEN full-length enriched library, clone:B130048J04 product:Eph receptor A3, full insert sequence.		
DE	Name=EphA3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Parthenogenote;		
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;		
RA	Carninci P., Hayashizaki Y.;		
RT	"High-efficiency full-length cDNA cloning.";		
RL	Meth. Enzymol. 303:19-44(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Parthenogenote;		
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;		
RA	RIKEN FANTOM Consortium;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Parthenogenote;		
RA	The FANTOM Consortium,		
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";		
RL	Nature 420:563-573(2002).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Parthenogenote;		
RX	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;		
RA	Kornio H., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,		
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";		
RL	Genome Res. 10:1617-1630(2000).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Parthenogenote;		
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;		
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,		
RT	"Normaliza-tion and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";		
RL	Genome Res. 10:1617-1630(2000).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Parthenogenote;		
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;		
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,		
RT	"Normaliza-tion and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";		
RL	Genome Res. 10:1617-1630(2000).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Parthenogenote;		
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;		
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,		
RT	"Normaliza-tion and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";		
RL	Genome Res. 10:1617-1630(2000).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Parthenogenote;		
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;		
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,		
RT	"Normaliza-tion and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";		
RL	Genome Res. 10:1617-1630(2000).		
RN	[5]		
RP			

13 LCYIWLIG--FAHTGE--AQAAKEVILLDSKAOQTELEWISSPPSGMEIISGLDENTYTP 67


```

Db      5 LSIIVLLGCCVLSGSGELSPQSPSNEVNLDSKTIQSGELGWTISPSHGWEKISGVDEHYTP 64
Qy      68 IRTYOVCGMBPNONNMRLRTNMISGNQRIFVELKFTLRCONSPGLGTCKEPEMLNY 127
Db      65 IRTYOVCGMBPNONNMRLRTNMISGNQRIFVELKFTLRCONSPGLGTCKEPEMLNY 124
Qy      128 YETDYDTGRNIRENLVYKIDITIADESFQGLGRKKKLNTVEVEIGPLSKKGYLAFO 187
Db      125 MESDDHGVKREHQFTKIDITIADESFQGLGRKKKLNTVEVEIGPLSKKGYLAFO 184
Qy      188 DVGACIALVSKYTKYKKWTIVENLAVPDTVTGSEBSLYLVNCTCYSAABEAEKSPR 247
Db      185 DVGACIALVSKYTKYKKWTIVENLAVPDTVTGSEBSLYLVNCTCYSAABEAEKSPR 241
Qy      248 MHGAEGBWLPVIGKCTICAKGYOOKGDTCEPCGRFRFYSSQDDQCSHCPTHSPSDEG 307
Db      242 MYCTGEGWLVPIGKCTICAKGYOOKGDTCEPCGRFRFYSSQDDQCSHCPTHSPSDEG 301
Qy      308 SRCECDGYRAPSDPPYVACTRPPSAPONLIPIINOTVLSLEMSPPADNGGRNDVTYRI 367
Db      302 MNCGCENNYFPAEADPEPMACTRPPSAPRNVISINETSVIDLMSWPLDTGGRDITFNI 361
Qy      368 LCKRCSMEQGEVCPGSGNIGMPQQTGLEDNVYVMDLIANAYTEVEAVNGVSDLSRS 427
Db      362 ICKKCGNMVROCEPCSPVNRFLPQLGLTNTVTVDLANTYTFEIDAVNGVSELSSP 421
Qy      428 ORLPAVSIITGOAPRQSVGVMKERVLRVQVLSMOBEPHPNVITTEYELKYEKQRE 487
Db      422 PROAAVSIITGOAPRQSVGVMKERVLRVQVLSMOBEPHPNVITTEYELKYEKQRE 481
Qy      488 RTVSTLTKTSASINNLKPGTVVFOIRAVTAAGYGYSPRLDVATLEASGKMFEXTA 547
Db      482 TSVTILARGNTVITSLKPTTYVFOIRAVTAAGYGYNSKFEPEISP-----DSFS 534
Qy      548 VSSSQNPVITIAVAVAGTIIIVFMVFGFTIGRRHCGYSKADQGDDEE-LYFHSLVNTEH 606
Db      535 ISGSHSVMIAMIAAVALIVLT--VTVYLVVGRFCGYHKSKEKRLHF---GNCH 588
Qy      607 LSV 609
Db      589 LKL 591

```

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RT      expressed."
CC      Oncogene 8:1807-1813(1993).
CC      - FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC      ephrin-A1, -A2, -A3, -A4 and -A5. Able to collapse growth cones.
CC      - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC      tyrosine phosphate.
CC      - SUBCELLULAR LOCATION: Type I membrane protein.
CC      - ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Comment=Additional isoforms seem to exist;
CC      Name=3;
CC      IsoId=P54755-1; Sequence=Displayed;
CC      Name=1;
CC      IsoId=P54755-2; Sequence=VSP_003005;
CC      Name=2;
CC      IsoId=P54755-3; Sequence=VSP_003004, VSP_003005;
CC      - TISSUE SPECIFICITY: Detected in the 10-day embryonic brain, weaker
CC      expression in the rest of the 10-day embryo. Undetected in adult
CC      tissues.
CC      - SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC      receptor subfamily.
CC      - SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC      - SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by, and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U03910; AAB0613.1; -.
DR      EMBL; U03910; AAB0612.1; -.
DR      EMBL; Z19058; CAA79508.1; -.
DR      PIR; I50615; I50615.
DR      HSSP; P54763; IUPA.
DR      InterPro; IPR006209; EGF like.
DR      InterPro; IPR001090; Ephrin_receptor.
DR      InterPro; IPR003961; FN_III.
DR      InterPro; IPR008957; FN_III-like.
DR      InterPro; IPR003962; FNIII subd.
DR      InterPro; IPR008979; Gal bind like.
DR      InterPro; IPR009030; Grow_fac_recept.
DR      InterPro; IPR011009; kinase like.
DR      InterPro; IPR000719; Prot_kinase.
DR      InterPro; IPR001660; SAM.
DR      InterPro; IPR001245; Tyr_kinase.
DR      InterPro; IPR008266; Tyr_kinase_AS.
DR      InterPro; IPR001426; YKase_receptorov.
DR      Pfam; PF01404; Ephrin_1bd; 1.
DR      Pfam; PF00041; Fn3; 2.
DR      Pfam; PF00069; Pkinase; 1.
DR      Pfam; PF00536; SAM; 1.
DR      PRINTS; PR00014; FNTYPEIIT.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD001495; Ephrin_receptor. 1.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00615; EPH_1bd; 1.
DR      SMART; SM00606; FN3; 2.
DR      SMART; SM00454; SAM; 1.
DR      SMART; SM00219; TYKc; 1.
DR      PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR      PROSITE; PS50853; FN3; 2.
DR      PROSITE; PS01017; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR      PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR      PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR      PROSITE; PS50105; SAM_DOMAIN; 1.
DR      KW      Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
KW      Receptor; Repeat; Signal; Transferrase; Transmembrane;

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KW Tyrosine-protein kinase.
FT SIGNAL 1 31
FT CHAIN 32 1013
FT DOMAIN 32 549
FT TRANSMEM 550 570
FT DOMAIN 571 1013
FT DOMAIN 196 330
FT DOMAIN 333 435
FT DOMAIN 445 535
FT DOMAIN 651 912
FT DOMAIN 941 1013
FT SITE 1011 1013
FT NP_BIND 657 665
FT BINDING 683 683
FT ACT_SITE 776 776
FT MOD_RES 626 626
FT MOD_RES 632 632
FT MOD_RES 809 809
FT MOD_RES 958 958
FT CARBOHYD 240 240
FT CARBOHYD 275 275
FT CARBOHYD 345 345
FT CARBOHYD 399 399
FT CARBOHYD 412 412
FT CARBOHYD 437 437
FT VARSPIC 280 443
FT VARSPIC 573 595
FT CONFLICT 981 1013
FT SEQUENCE 1013 AA; 112245 MM; AC36FDAEBF38382 CRC64;

Query Match 55.6%; Score 1802; DB 1; Length 1013;
Best Local Similarity 55.3%; Pred. No. 2,4e-126;
Matches 347; Conservative 96; Mismatches 137; Indels 48; Gaps 10;

8 PSM--IILCYIMLGFPHTEBAQAQAVLLDSQAQTELEWISSPSCGEISGLDENTY 65
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
15 PGMTCULLCALBSLSPG-----SEVNLLDSRTVWDGWLAYPKNGEBEIGEDENY 69
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
66 TPRTYOVCOVMEPNQNNMLRTNMISKGNQRIEVLKFTLPDQNSLPGVIGCKEPENL 125
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
70 APIHTYOVCKVMEQNNMLLTISWISNEGPPASSFELKFTLRDQNSLPGLGCKETENM 129
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
126 YVYETDYTGRTIRENLVYKIDITIADESFTQDGLGERKMLTEVEREIGPLSKGFYLA 185
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
130 YFESDEDEDGRNIRENGYIKIDITIADESFTELDGRVWKLNTVEVDVCLTKKGYLA 189
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
186 FQVVGACIALVSKYVKKKWTIVENLAVRPDYTGSEFSLYEVKTCYS-SAEAEAN 244
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
190 FQVVGACIALVSKYVKKKWPVRLARPPDITIGADSQQLLEVSGVCAVNSTLFEA-- 247
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
245 SPMHSGAGEEMLVPIGKCIKAGYQOKGPTCEFCGRGFRKSSQDQGCRCPTHSFSR 304
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
248 -PKMHGASGEMLVPIGKCIKAGYQOKGPTCEFCGRGFRKSSQDQGCRCPTHSFSR 306
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
305 EGSSRCCEBDGYRAPSPDYVACTRPPSAPONLFINQNTVSLSEMSPADNGRNDVT 364
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
307 EASTSGCCEHYFRRESDDPTMACTRPSPASISVNFETSVLEWIPFADVGRKDV 366
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
365 YRLICRCSMEQGEVCGSNIGMPQGTGLEDNYTVMLLAHANTTFVEAVNGVSD 424
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
367 YYLACKKCNHSGICEACGSHVRLPQGTGKNTSVMMVDDLHNTNTFRIEAVNGVSDQ 426
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
425 SRSQRLFAAASITTTGAAPSOVSGVMKERYLORSVOLSMQEPHENVIVTEYETKYEKD 484
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
427 NPGARQPFVSNVTTNOAAPSPVSSVKKGKITKNSISLSMQEPDRPNCIILIEYETKFEKD 486

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QY 485 QERITYSLTKTKTSASINNLKPGTYVYFQIRAVTAAGYGNVSPRLDVATLEBASGMFE 544
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 487 Q-ETSYTIIRKSKETATLADLKFSGASVVFQIRARTAGYGGFRRREFET-----SP 537
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 545 ATAVSSEQNPTIIVAVNAVGTIIIVPMVPGFIIGR-----H 582
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 538 VLAASDQSQIPIT-VSVTVGVILLAVIGFILSGSCDCHGCGMASLRAVAPSLIMR 596
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 583 CGYSKADQEGDEE-LYFHSILVTEHLSV 609
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 597 CGYSKAKQDEERKMFFH-----NGHKL 620
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 14
ID EP33 HUMAN STANDARD; PRT; 983 AA.
AC P29320; Q9H2V3; Q9H2V4;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor ETK1) (HEK4).
GN Name=EP33; Synonyms=ETK, ETK1, HEK,
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxId=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=92179233; PubMed=1311845;
RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine
RT kinase expressed by human lymphoid tumor cell lines.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Melanoma;
RX MEDLINE=20441582; PubMed=10987298;
RA Chlari R., Hames G., Stroobant V., Texter C., Maille B., Boon T.,
RA Coulie P.G.;
RT "Identification of a tumor-specific shared antigen derived from an Eph
RT receptor and presented to CD4 T cells on HLA class II molecules.";
RL Cancer Res. 60:4855-4863(2000).
RN [3]
RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
RX MEDLINE=92147681; PubMed=1737782;
RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A.,
RA Welch K., Loudovaris M., Rockman S., Bushmanis I.;
RT "Isolation and characterization of a novel receptor-type protein
RT tyrosine kinase (hek) from a human pre-B cell line.";
RL J. Biol. Chem. 267:3262-3267(1992).
RN [4]
RP SGLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC -!- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC ephrin-A2, -A3, -A4 and -A5. Could play a role in lymphoid
CC function.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC -!- SECRETED (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P29320-1; Sequence=Displayed;
CC Note=May be produced at very low levels due to a premature stop
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC Name=2;
CC IsoId=P29320-2; Sequence=VSP_002995, VSP_002996;

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OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RA Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_taxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Deje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
 RA Datchenko L., Madan A., Marasa K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pierce C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley P.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pailey J., Heltou E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley A.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
 RA Krywinski M., Marra M.A.,
 RA Jones S.U., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity) .
 CC -I- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 CC receptor subfamily.
 CC EMBL; BC063282; AAH63282.1; -.
 DR HSSBP; P54763; IKGy.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005503; F:ephrin receptor activity; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA
 DR InterPro; IPR0060309; BGF_1like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003962; Ftn11_subd.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-1like.
 DR InterPro; IPR008979; Gal_bind_1like.
 DR InterPro; IPR011009; Kinase_1like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR011510; SAM_2.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; Ykase_receptorlv.
 DR Pfam; PF01404; Ephrin_1bd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF07647; SAM_2; 1.
 DR PRINTS; PR00014; FNTYPEP11.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000003; Prot_kinase; 1.
 DR SMART; SM00615; EPH_1bd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00220; S_TKC; 1.

DR SMART; SMO0219; TYRK; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50853; EN3; 2.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS50195; SAM_DOMAIN; 1.
KM ATP-binding; Glycoprotein; kinase; phosphorylation; Receptor;
KM transase; transmembrane; tyrosine-protein kinase.
SQ SEQUENCE 963 AA; 110160 MW; 1EBDABFC59282527 CRC64;

Query Match	55.5%	Score 1799:	DB 2	Length 983:
Best Local Similarity	57.0%	Pred. No. 3.8e-126:		
Matches 332:	Conservative 103:	Mismatches 131:	Indels 16:	Gaps 6
QY	28	QAAKEVLLDLSKAQOOLEWMISSPPSGMEIISGLDENTYPIRTYQVOCVMEPNQNMWLT	87	
DB	25	QPSNEVNLDDSKTIQGLGEMISYPSHGMEIISGVDEHYTPRTYQVCMVMDHSQNMWLT	84	
QY	88	NWISKANQRI.FVELKFTLRDQNSLPGVLCGCKETPNLYYETDYDGRNIRENLYVAD	147	
DB	85	NWVPNRSQKRIYELKFTLRDQNSIPLVLGCKETPNLYYMSDDHGVKREHQFTIAD	144	
QY	148	TTAADESTFQDLDSEGRKKMLNTEVREIPIPLSKSGFYLAFOVGACIALVSVKYYKKCMT	207	
DB	145	TTAADESTFQDLDLGRILKNTETIREVGPVKKGFYLAFOVGACIALVSVRVYFKKCP	204	
QY	208	IVENLAIVPDTVTGSEPSISVEVGTQVSAEELAEHNSPRMCSAEGEMVLPIGCKTCA	267	
DB	205	TVKNILAMPDPTVP--MDSQSLVEVAGSCVNNKSKE--EDPEPMYCSGTEGEMVLPIGCKSCNA	261	
QY	268	GYQCKGDTCECGCGRRFYKSSSQDILQCSRCPIHPSFSDRGSSRCCEQGYVAPASDPPEVA	327	
DB	262	GYEERGFQCAQCRPGFYALDGNKKCAACCPHSSSTQEDGSMNCKENNYFPADKQPSMA	321	
QY	328	CTRPSPAPQNLIFINQTTVLSLEMSPRADNGRNDVTYRLICKRCSWQCEGCPVCSNIG	387	
DB	322	CTRPSPSPRNVIINSINETSVLDMSPWLDIGRQDVFNIIICKCGMWIKQCEPCSPMYR	381	
QY	388	YMPQOTGLIEDYVTVMDLIAHANTTFEVEAVNGVSDLSRQRLPAVSIITGQAAPSOVS	447	
DB	382	FLRPGFGTLNNTVVTDLIAHTNTTFELIDAVNGVSELSPPROPAAVSIITNOAPSVEL	441	
QY	448	GWMEKRVLOBSVOLSMOEPHPNGVITTELYKYEKOOREBTGYLTKTKSASINNLKP	507	
DB	442	TYKQDRISRNSISLSMOEPHPNGIILDYKXYTEKQOEQESTYTLRARGNVTISLKP	501	
QY	508	GTVVVYFOIRATYAAGYNGYSPRLDVATLDEASGKFEATAVSSEONPVIIIAVVAVACTI	567	
DB	502	DTIVVFOIRATYAAGYGTNSRKKPEPISP-----DFSISGESSQVMIATISAVALI	554	
QY	568	ILVEMVFGITIGRRHCGSKADQEGDEBELYHSLVTNENHLSV	609	
DB	555	ILTVIVY-VLIG-RFCGYSKHGADKKRLHF-----GNGHLLK	590	

Search completed: August 23, 2005, 08:30:04
Job time : 73.5744 secs

DR SMART; SM00220; S TKC; 1.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:30:14 ; Search time 109.563 Seconds
(without alignments)
2180.182 Million cell updates/sec

Title: US-10-073-064-3
Perfect score: 3243
Sequence: 1 MVQTRPSPWIIICYLWLG.....EGDELYHSLVTEHLSVL 610

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications RA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppaa/US09C_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US10E_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubppaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3191	98.4	998 10 US-09-823-187-42	Sequence 42, Appl
2	3175	97.9	998 10 US-09-823-187-43	Sequence 43, Appl
3	3139	96.8	945 15 US-10-112-944-260	Sequence 260, Appl
4	3139	96.8	998 10 US-09-823-187-40	Sequence 40, Appl
5	3031.5	93.5	993 10 US-09-823-187-39	Sequence 39, Appl
6	3031.5	93.5	993 10 US-09-823-187-41	Sequence 41, Appl
7	1843	56.8	991 10 US-09-823-187-44	Sequence 44, Appl
8	1838.5	56.7	1041 18 US-10-840-512-215	Sequence 215, Appl
9	1832.5	56.5	953 14 US-10-412-277-7	Sequence 7, Appl
10	1829	56.4	991 17 US-10-732-923-13667	Sequence 13667, A
11	1821	56.2	1005 15 US-10-029-020-63	Sequence 63, Appl

12	1819	56.1	1037 14 US-10-316-124-3	Sequence 3, Appl1
13	1819	56.1	1037 15 US-10-353-690-40	Sequence 40, Appl1
14	1819	56.1	1037 20 US-11-064-551-3	Sequence 3, Appl1
15	1808.5	55.8	975 14 US-10-412-277-8	Sequence 8, Appl1
16	1802	55.6	1013 17 US-10-412-277-8	Sequence 13668, A
17	1799	55.5	666 9 US-09-771-161A-136	Sequence 136, App
18	1799	55.5	983 4 US-09-771-161A-227	Sequence 227, App
19	1799	55.5	983 14 US-10-205-823-97	Sequence 97, Appl
20	1799	55.5	983 14 US-10-345-680-2	Sequence 2, Appl1
21	1799	55.5	983 15 US-10-295-020-602	Sequence 602, App
22	1799	55.5	983 15 US-10-029-020-59	Sequence 59, Appl
23	1799	55.5	983 17 US-10-794-514A-467	Sequence 467, App
24	1799	55.5	983 18 US-10-489-125B-11	Sequence 11, Appl
25	1788.5	55.1	985 15 US-10-029-020-61	Sequence 61, Appl
26	1786.5	55.1	968 14 US-10-412-277-6	Sequence 6, Appl1
27	1786.5	55.1	983 17 US-10-732-923-13675	Sequence 13675, A
28	1736.5	53.5	921 9 US-09-805-020-52	Sequence 52, Appl
29	1736.5	53.5	986 16 US-10-723-860-597	Sequence 597, App
30	1729.5	53.3	1104 9 US-09-982-610-36	Sequence 36, Appl
31	1701.5	52.5	935 15 US-10-449-569-36	Sequence 5, Appl1
32	1701.5	52.5	992 10 US-09-973-424A-53	Sequence 53, Appl
33	1701.5	52.5	992 17 US-10-691-165-5	Sequence 5, Appl1
34	1701.5	52.5	992 17 US-10-691-165-5	Sequence 53, Appl
35	1701.5	52.5	992 17 US-10-691-165-53	Sequence 2, Appl1
36	1701.5	52.5	1005 15 US-10-449-569-2	Sequence 3, Appl1
37	1701.5	52.5	1012 15 US-10-168-582-3	Sequence 34, Appl
38	1699.5	52.4	935 15 US-10-449-569-34	Sequence 52, Appl
39	1695	52.3	991 10 US-09-973-424A-52	Sequence 52, Appl
40	1695	52.3	991 17 US-10-691-165-52	Sequence 52, Appl
41	1676	51.7	1035 15 US-10-029-020-20	Sequence 20, Appl
42	1670.5	51.5	1036 14 US-09-971-708-2	Sequence 2, Appl1
43	1670.5	51.5	1036 14 US-10-245-752-104	Sequence 104, App
44	1670.5	51.5	1036 14 US-10-245-859-104	Sequence 104, App
45	1670.5	51.5	1036 14 US-10-245-103-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-09-823-187-42
; Sequence 42, Application US/09823187
; Publication No. US20030096952A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine
APPLICANT: Gusev, Vladimir Y
APPLICANT: Liu, Xiaohong
APPLICANT: Majumder, Kund
APPLICANT: Paturajan, Muralidhar
APPLICANT: Paturajan, Meera
APPLICANT: Shinkets, Richard A
APPLICANT: Spaderna, Steven K
APPLICANT: Spytek, Kimberly
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/423,187
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,081

; PRIOR FILING DATE: 2000-04-13
 ; PRIOR APPLICATION NUMBER: 60/197,525
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/197,087
 ; PRIOR FILING DATE: 2000-04-14
 ; NUMBER OF SEQ ID NOS: 103
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 42
 ; LENGTH: 998
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-823-187-42

Query Match 98.4%; Score 3191; DB 10; Length 998;
 Best Local Similarity 100.0%; Pred. No. 6,7e-244;
 Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVVOTRPPSWIILCYIMLGFHAGTGAQAQAEVILLDSKAQOQTELEWISSPPSGMEISG	60
Ds	1	MVVOTRPPSWIILCYIMLGFHAGTGAQAQAEVILLDSKAQOQTELEWISSPPSGMEISG	60
Qy	61	LDENVYTPRTYQVQVMEPNQNMWLRNMTSKGNAORIFVELKFTLRDCKSLPGLGTCK	120
Ds	61	LDENVYTPRTYQVQVMEPNQNMWLRNMTSKGNAORIFVELKFTLRDCKSLPGLGTCK	120
Qy	121	ETFNLYYETDYGTRNIRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGPLSKK	180
Ds	121	ETFNLYYETDYGTRNIRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGPLSKK	180
Qy	181	GFYLAPODVACIALVSVKYYKKCMTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAE	240
Ds	181	GFYLAPODVACIALVSVKYYKKCMTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAE	240
Qy	241	EAEKSPRMHCSAEGEMVLPIGKCIKAGYQOKGDTCEPCGRFRYKSSSOLQCSRCPHIS	300
Ds	241	EAEKSPRMHCSAEGEMVLPIGKCIKAGYQOKGDTCEPCGRFRYKSSSOLQCSRCPHIS	300
Qy	301	FSDREGSSRCECDGYRAPSDPPYVACTRPAPAPNLIENINQTVLSLEWSPADNGR	360
Ds	301	FSDREGSSRCECDGYRAPSDPPYVACTRPAPAPNLIENINQTVLSLEWSPADNGR	360
Qy	361	NDVTYRILCKRCSEWQEGECVPCGSGNIGMPQOTGLDNTYVMDLLAHANTFEVEAVNG	420
Ds	361	NDVTYRILCKRCSEWQEGECVPCGSGNIGMPQOTGLDNTYVMDLLAHANTFEVEAVNG	420
Qy	421	VSDLSRSQRLFAAVSITGGAAPSOVSGWKEVLRQSVOLSWQEPHHPGVITEYEIKY	480
Ds	421	VSDLSRSQRLFAAVSITGGAAPSOVSGWKEVLRQSVOLSWQEPHHPGVITEYEIKY	480
Qy	481	YEKQRERTYSTLTKSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVATLLEASG	540
Ds	481	YEKQRERTYSTLTKSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVATLLEASG	540
Qy	541	KMEFATVASEQNPVILIAVAVAGTIIIVFVFGFIIGRRHCGYSKADCEGDELYFH	599
Ds	541	KMEFATVASEQNPVILIAVAVAGTIIIVFVFGFIIGRRHCGYSKADCEGDELYFH	599

RESULT 2

; Sequence 43, Application US/09823187
 ; Publication No. US20030096952A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Gusev, Vladimir Y
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Majumder, Kumud
 ; APPLICANT: Padigaru, Muralidhar
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Spaderna, Steven K
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Taupier, Raymond J

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 15966-745
 ; CURRENT APPLICATION NUMBER: US/09/823,187
 ; CURRENT FILING DATE: 2001-03-29
 ; PRIOR APPLICATION NUMBER: 60/193,339
 ; PRIOR FILING DATE: 2000-03-30
 ; PRIOR APPLICATION NUMBER: 60/193,205
 ; PRIOR FILING DATE: 2000-03-30
 ; PRIOR APPLICATION NUMBER: 60/195,343
 ; PRIOR FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: 60/195,088
 ; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: 60/195,005
 ; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: 60/195,792
 ; PRIOR FILING DATE: 2000-04-10
 ; PRIOR APPLICATION NUMBER: 60/196,556
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: 60/197,081
 ; PRIOR FILING DATE: 2000-04-13
 ; PRIOR APPLICATION NUMBER: 60/197,525
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/197,087
 ; NUMBER OF SEQ ID NOS: 103
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 43
 ; LENGTH: 998
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-823-187-43

Query Match 97.2%; Score 3175; DB 10; Length 998;
 Best Local Similarity 99.2%; Pred. No. 1.2e-242;
 Matches 594; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MVVOTRPPSWIILCYIMLGFHAGTGAQAQAEVILLDSKAQOQTELEWISSPPSGMEISG	60
Ds	1	MVVOTRPPSWIILCYIMLGFHAGTGAQAQAEVILLDSKAQOQTELEWISSPPSGMEISG	60
Qy	61	LDENVYTPRTYQVQVMEPNQNMWLRNMTSKGNAORIFVELKFTLRDCKSLPGLGTCK	120
Ds	61	LDENVYTPRTYQVQVMEPNQNMWLRNMTSKGNAORIFVELKFTLRDCKSLPGLGTCK	120
Qy	121	ETFNLYYETDYGTRNIRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGPLSKK	180
Ds	121	ETFNLYYETDYGTRNIRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGPLSKK	180
Qy	181	GFYLAPODVACIALVSVKYYKKCMTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAE	240
Ds	181	GFYLAPODVACIALVSVKYYKKCMTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAE	240
Qy	241	EAEKSPRMHCSAEGEMVLPIGKCIKAGYQOKGDTCEPCGRFRYKSSSOLQCSRCPHIS	300
Ds	241	EAEKSPRMHCSAEGEMVLPIGKCIKAGYQOKGDTCEPCGRFRYKSSSOLQCSRCPHIS	300
Qy	301	FSDREGSSRCECDGYRAPSDPPYVACTRPAPAPNLIENINQTVLSLEWSPADNGR	360
Ds	301	FSDREGSSRCECDGYRAPSDPPYVACTRPAPAPNLIENINQTVLSLEWSPADNGR	360
Qy	361	NDVTYRILCKRCSEWQEGECVPCGSGNIGMPQOTGLDNTYVMDLLAHANTFEVEAVNG	420
Ds	361	NDVTYRILCKRCSEWQEGECVPCGSGNIGMPQOTGLDNTYVMDLLAHANTFEVEAVNG	420
Qy	421	VSDLSRSQRLFAAVSITGGAAPSOVSGWKEVLRQSVOLSWQEPHHPGVITEYEIKY	480
Ds	421	VSDLSRSQRLFAAVSITGGAAPSOVSGWKEVLRQSVOLSWQEPHHPGVITEYEIKY	480
Qy	481	YEKQRERTYSTLTKSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVATLLEASG	540
Ds	481	YEKQRERTYSTLTKSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVATLLEASG	540
Qy	541	KMEFATVASEQNPVILIAVAVAGTIIIVFVFGFIIGRRHCGYSKADCEGDELYFH	599

Db 541 KMFEATAVSSSEQNPV11IAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599

RESULT 3

US-10-112-944-260
Sequence 260, Application US/10112944
Publication No. US20040048249A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Zheng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT FILING DATE: 2002-07-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000/01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pf_fl_genes Version 5.0
SEQ ID NO 260
LENGTH: 945
TYPE: PRT
ORGANISM: Homo sapiens
US-10-112-944-260

Query Match 96.8%; Score 3139; DB 15; Length 945;

Best Local Similarity 97.7%; Pred. No. 8.3e-240; Mismatches 4; Indels 0; Gaps 0;

Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVTQRFPSWIIICITWILGFAHTGEAQAQAEVLLDSKAQOTLEWISSPPSGWEISG 60
DB 1 MVTQRFPSWIIICITWILGFAHTGEAQAQAEVLLDSKAQOTLEWISSPPSGWEISG 60
QY 61 LDENVTPRTYOVQCVMEPNONNMLRTNWKSKNAQRIFEVLKFTLRDQNSLPVGLGTCK 120
DB 61 LDENVTPRTYOVQCVMEPNONNMLRTNWKSKNAQRIFEVLKFTLRDQNSLPVGLGTCK 120
QY 121 ETPNLYYETDYGGRNIRENLYVKIDTIADESFQDGLGBRKKKNTVEIREIGPLSKK 180
DB 121 ETPNLYYETDYGGRNIRENLYVKIDTIADESFQDGLGBRKKKNTVEIREIGPLSKK 180
QY 181 GFYLAFOVGAICALVSVKVVYKKCWITVENLAIVPDTVTGSESSSLVEVAGTCVSSAEE 240
DB 181 GFYLAFOVGAICALVSVKVVYKKCWITVENLAIVPDTVTGSESSSLVEVAGTCVSSAEE 240
QY 241 EAENSPPRHGASGEMWLVPIGKCTICKAGYQOKGDTCEPCGRRFYKSSQDILQCSRCPHHS 300
DB 241 EAENSPPRHGASGEMWLVPIGKCTICKAGYQOKGDTCEPCGRRFYKSSQDILQCSRCPHHS 300

QY 301 FSDREGSSRCECEDGYRAASDPPIVACTRPPSAPQNLIFINQTVLSLEMSPPADNGCR 360
DB 301 FSDREGSSRCECEDGYRAASDPPIVACTRPPSAPQNLIFINQTVLSLEMSPPADNGCR 360
QY 361 NDVTYRILCKRCSMEQCEVPCGSGNIGYMPQOTGLEDNYVTVMDLAHANTFEVEAVNG 420
DB 361 NDVTYRILCKRCSMEQCEVPCGSGNIGYMPQOTGLEDNYVTVMDLAHANTFEVEAVNG 420
QY 421 VSDLSRQRLFAAIVSTTGAAPSOVSGWKEKRLQSRNLSKQEPHEPNVITEYEIKY 480
DB 421 VSDLSRQRLFAAIVSTTGAAPSOVSGWKEKRLQSRNLSKQEPHEPNVITEYEIKY 480
QY 481 YEKQRERTYSTLTAKGTSASINNLKPGTYVYVQIRAVTAAGYGNYSFRLDVATLEASG 540
DB 481 YEKQRERTYSTLTAKGTSASINNLKPGTYVYVQIRAVTAAGYGNYSFRLDVATLEASG 540
QY 541 KMFEATAVSSSEQNPV11IAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599
DB 541 KMFEATAVSSSEQNPV11IAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599

RESULT 4

US-09-823-187-40
Sequence 40, Application US/09823187
Publication No. US20030096952A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine
APPLICANT: Gusev, Vladimir Y
APPLICANT: Liu, Xiaohong
APPLICANT: Majumder, Kumud
APPLICANT: Padigaru, Muralidhar
APPLICANT: Patturajan, Meera
APPLICANT: Shinkets, Richard A
APPLICANT: Spaderna, Steven K
APPLICANT: Spytek, Kimberly
APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/823,187
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,081
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,525
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/197,087
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 998
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-187-40

Query Match 96.8%; Score 3139; DB 10; Length 998;

Best Local Similarity 97.7%; Pred. No. 9e-240; Mismatches 4; Indels 0; Gaps 0;

Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MMVOTRPSMIIICVIMLGFAGHTGAQAKVLLDSQAQOTLEMISSPSCGMEETSG	60
Db	1	MVFOTRPSMIIICVIMLGFAGHTGAQAKVLLDSQAQOTLEMISSPSCGMEETSG	60
Qy	61	LDENVYTRIRYQVCQVMEPQNMMLETRNNISKGNQRIPEVLEKFTLRONSIPVGLGTC	120
Db	61	LDENVYTRIRYQVCQVMEPQNMMLETRNNISKGNQRIPEVLEKFTLRONSIPVGLGTC	120
Qy	121	ETPNLYYEFNDYDTGNIRENLVYKIDTTAADEFTQDGLGRKKMLTEVREIGPLSKK	180
Db	121	ETPNLYYEFNDYDTGNIRENLVYKIDTTAADEFTQDGLGRKKMLTEVREIGPLSKK	180
Qy	181	GFYLAPODVACIALVSVKYKYYKKMTIENLAVPDTVTSEPSFLNEVGTCVSSAE	240
Db	181	GFYLAPODVACIALVSVKYKYYKKMTIENLAVPDTVTSEPSFLNEVGTCVSSAE	240
Qy	241	EAENSPPMHCSAEGEMLVPIGKICICAGYQOKGDTPECGRGRFYSSSDIQCSCRPTH	300
Db	241	EAENAPPMHCSAEGEMLVPIGKICICAGYQOKGDTPECGRGRFYSSSDIQCSCRPTH	300
Qy	301	FSDEGSSRCECEDGYIRAPSDPYPVYACTRPPSAPONLIFINQTTVSLVSPPADNGR	360
Db	301	FSDEGSSRCECEDGYIRAPSDPYPVYACTRPPSAPONLIFINQTTVSLVSPPADNGR	360
Qy	361	NDVYTRILCKRCSEMEGECIPGCSNIGYMPQOTGLEDNYTMDLAAANTFEVEANG	420
Db	361	NDVYTRILCKRCSEMEGECIPGCSNIGYMPQOTGLEDNYTMDLAAANTFEVEANG	420
Qy	421	VSDLSRQRLFAAVSITTGQAAPSOVSGVWKEKRVLORSVLSMOPEHPNKVITEYEIKY	480
Db	421	VSDLSRQRLFAAVSITTGQAAPSOVSGVWKEKRVLORSVLSMOPEHPNKVITEYEIKY	480
Qy	481	YEKQORERTYSTLKTSKTSASINMLKPTVYVFOJAAVTAAGYGNYSRPLIVATLEBASG	540
Db	481	YEKQORERTYSTLKTSKTSASINMLKPTVYVFOJAAVTAAGYGNYSRPLIVATLEBASG	540
Qy	541	KMFPAATVSSQNPVIIIAVVAAGTIIIVFWFGIIIGRRHCGYSKADQGDDELYFH	599
Db	541	KMFPAATVSSQNPVIIIAVVAAGTIIIVFWFGIIIGRRHCGYSKADQGDDELYFH	599

	/ PRIOR FILING DATE: 2000-04-11	
	/ PRIOR APPLICATION NUMBER: 60/197,081	
	/ PRIOR FILING DATE: 2000-04-13	
	/ PRIOR APPLICATION NUMBER: 60/197,525	
	/ PRIOR FILING DATE: 2000-04-14	
	/ PRIOR APPLICATION NUMBER: 60/197,087	
	/ PRIOR FILING DATE: 2000-04-14	
	/ NUMBER OF SEQ ID NOS: 103	
	/ SOFTWARE: PatentIn Ver. 2.1	
	/ SEQ ID NO 39	
	/ LENGTH: 993	
	/ TYPE: PRT	
	/ ORGANISM: Gallus gallus	
	US-09-823-187-39	
Query Match	93.5%; Score 3031.5; DB 10; Length 993;	
Best Local Similarity	94.5%; Pred. No. 3e-231;	
Matches 566; Conservative 17; Mismatches 11; Indels 5; Gaps 1,		
OY	1 MVOTRFPSSWILLCIYLWGPAHNGEAOAAKEVLLDSKQAOTELEWISSPPSGMEETISG	60
Dd	1 MYLSRLPFWIMLCSVLIRFAHTGEQAAAKEVILLDSKAQOTELEWISSPPNGMEETSIG	60
OY	61 LDENVTPRTYOVOOVNEPNOMMLRTMWSISKNAORFVFLKFTLRPCNSLPGLGTCK	120
Dd	61 LDEVNTPIRYTOVCOWMESNONMWLRMTWLAKSNARLEVLFKFTLRPCNSLPGLGTCK	120
OY	121 ETPLNYEETDYDGRNIRENLVVKIDTIADESFTGGDLGERMKLTVEARELGPSLK	180
Dd	121 ETFNLYYEITDYDGRIINREMGYVKIDTIADESFSTGGDLGERMKLTVEARELGPSLK	180
OY	181 GFYLAPODVGAIALVSIVKYKKCWTVENLAVPDTVTGSSEFSLVETRGTCVSAEE	240
Dd	181 GFYLAFOVGACIALVSIVKYKKCWSIIENLAFPDVTGVSEFSSLVEVRGTCVSAEE	240
OY	241 EAENSPRHGCAEBEWLVPGIKCI CKAGYOOKGDTCBPCCGRFFXSSGODLOCSCPTH	300
Dd	241 EAENSPKHGCSABEGWLVPIGKCICAKGYOOKGDTCBPCCGCFYKSSQDLQCRCPTH	300
OY	301 FSDEGSGSRCEBDEGGYYPAPSDPYVACTRPASAPONLI FININTVTSLEWSPPADNGR	360
Dd	301 FSDGESSRGDCEDSYRYAPSDPHYVACTRRPASAPONLI FININTVTSLEWSPADNGR	360
OY	361 NDVTYTRILCKRCSMEOGECVPCCSNI GMPOQTGLENDYVTVMDLHAANYTFVEAYNG	420
Dd	361 NDVTYTRILCKRCSMEOGECVPCCSNI GMPOQTGLVDNVTVTMLAHANATFEVEAYNG	420
OY	421 VDSLRSQRLLFAAYSITTGOAAPBOVSGVMERVLORSVOLSMODEPHNVIITEYEIKY	480
Dd	421 VSDSLRSQRLLFAAYSITTGOAAPQSVSWMERVLORVELSMODEPEHPNVITIEYEIKY	480
OY	481 YEKOREERTYSTLTKTKSTSASINNLKPITYVVFQIRATAAGYNVSPRLDATLEEASG	540
Dd	481 YEKOREERTYSTVTKTKSTSASINNLKGTYVVFQIRATAAGYGNISRKLDAVILEERT-	539
OY	541 KMFETAIVASSEQNPIIIIAVAAGAATTILVMEFGFIIGRHCGSKADQGDEELFYH	599
Dd	540 ----ATAVASSEQNPVIIIAVAAGAATTILVFMVFGFIIGRHCGSKADQGDEELYH	594
RESULT 6		
	US-09-823-187-41	
	/ Sequence 41, Application US/09823187	
	/ Publication No. US2003009652A1	
	/ GENERAL INFORMATION:	
	/ APPLICANT: Burgess, Catherine	
	/ APPLICANT: Gusev, Vladimlr Y	
	/ APPLICANT: Liu, Xiaohong	
	/ APPLICANT: Majumder, Kumud	
	/ APPLICANT: Padigaru, Muralidhar	
	/ APPLICANT: Patnurajan, Meera	
	/ APPLICANT: Shinkets, Richard A	
	/ APPLICANT: Spaderna, Steven K	

[illegible]

DD 100 LAF QDVGALVSVKVIKUCFSV

DB	100	120	140	160	180	200	220	240	260	280	300	320	340	360	380	400	420	440	460	480	500	520	540	560	580	600	620	640	660	680	700	720	740	760	780	800	820	840	860	880	900	920	940	960	980	1000
DB	100	120	140	160	180	200	220	240	260	280	300	320	340	360	380	400	420	440	460	480	500	520	540	560	580	600	620	640	660	680	700	720	740	760	780	800	820	840	860	880	900	920	940	960	980	1000

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184 LAFQDVACIALSVKVVYKKKCWTIVENTLAVFPDPTVTGSEFSSLVBEVRGTCVSSAEEAE 243
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
188 LAFQDVACIALSVRVVYKKCPSVVRHLAVFPDITIGADSSQLLEVGSGCN--HSVTD 245

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QY 244 NSPRMCSAEGEWLVPICKICIKAGYQOKGDTCEPCGRFRFYKSSSDQLQCS 303
DB 246 EPRMHCASAGEMLVPIGKCMCKRAGYEKNGTCOVCPRGFFKASPHIQSCGKCPHXYTH 305
QY 304 REGSSRECEDEGYRAPSDDPYVACTRPPAPQULININQTYSLFMSPPANDGENDV 363
DB 306 EASSTCVCEKDYFRRESDDPTVMACTRPPAPRAISNVNSETSFLFWIPADGGKADV 365
QY 364 TYRILCRCSWEOGECVPCSGNIGMPQOTGLBNDYTVMDLLAHANYTEEVEAVNGVSD 423
DB 366 SYTLACKCKSHAGVCECGHVRYLPRQGLKNTSVMAMDLLAHNTYTEIEAVNGVSD 425
QY 424 LSRNQRLPAVSTTGGAPSOVSQWKEKRYLQSRVOLSWOEPHPNGVITTEIKYEEK 483
DB 426 LSPBARQVSVNVTNNQAAPSPTVNNKKGKIAKXISLSWQEPDRPNGIILLEYEIKHEK 485
QY 484 DQERETSTLKTSTASINNLKGTYYVQIARVTAAGYNGVSPRLDVATLEBASGMF 543
DB 486 DQ-ETSTYTIKSKETITLTAEGLKASVYVQIARVTAAGYNGVSPRLDVATLEBASGMF 543
QY 544 EAT---AVSEQNPVITIAVAVAGTIIIVFVWGFIIGRRHCGSKADQGDDE-LYFH 539
DB 534 ETTPVFASSDQSQIPVIAVSVTWG-VILLAVIGVLISGRRCYSKAKOLPEEKMHFH 532
QY 600 SLVTNHLV 609
DB 593 ----NGHIKL 598

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RESULT 8
US-10-840-512-215
; Sequence 215, Application US/10840512
; Publication No. US20050125852A1
; GENERAL INFORMATION:
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: MANNING, GERARD
; APPLICANT: CHARIDCZAK, GLEN
; APPLICANT: GRIGORIEV, IGOR
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-1455
; CURRENT APPLICATION NUMBER: US/10/840, 512
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469, 014
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215
; LENGTH: 1041
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-840-512-215

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Query Match 56.7%; Score 1838.5; DB 18; Length 1041;
Best Local Similarity 54.8%; Pred. No. 1.5e-136;
Matches 352; Conservative 98; Mismatches 135; Indels 57; Gaps 11;

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QY 6 RPSMWILCY-----IW-----LIGRAHTGEAQAQAEVLLDLSKAQOTLEWISSPPSG 54
DB 25 RVAPSLAGCYSAPLAKGLWLCULLCALRTLILASPSNEVNLDBSRITWGLGWIAPFKNG 84
QY 55 WEETSGIDENYTPRTTYQVCVNEPNONNMLRTNWSKGNAGRI FVELKTTLRDONS LFG 114
DB 85 WEETGEVDENYAPHTHYQVCKMEONNNMLTSMISNEGASRI FIELKFTLRDONS LFG 144
QY 115 VLIGCKETPLUYVYETDYDGRNIRENLVYKIDITLADSFQSGDGERMGLNTEVREI 174
DB 145 GLIGCKETPLUYVYETDYDGRNIRENLVYKIDITLADSFQSGDGERMGLNTEVREI 204
QY 175 GPLSKGFFYLAFOVAGACIALVSVKYYKKCWTIVENLAVFPDVTGSESSSLVEVAGTC 234
DB 205 GPLSKGFFYLAFOVAGACIALVSVKYYKKCPSVVRRLAIFPDITITADE SQLLEVSGSC 264
QY 235 VSSAEBEASNSPRMHCASAGEMLVPIGKICIKAGYQOKGDTCEPCGRFRFYKSSSDQLQCS 294

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DB 265 VN--HSVTDDPPRPMHCASAGEMLVPIGKCMCKRAGYEKNGTCOVCPRGFFKASPHISQOTS 322
QY 295 RCPTHSFSDREGSSRECEDEGYRAPSDDPYVACTRPPAPQULININQTYSLFMSPP 354
DB 323 KCPPHSYTHEASTCVCEKDYFRKSDPTVMACTRPPAPRAISNVNSETSFLFWIP 382
QY 355 ADNGRNDVYRILCRCSWEOGECVPCSGNIGMPQOTGLBNDYTVMDLLAHANYTEE 414
DB 383 ADTGRKDVSYTYLACKCKNSHAGVCECGHVRYLPRQGLKNTSVMAMDLLAHNTYTE 442
QY 415 VEAVNGVSDLSRQRLPAVSTTGGAPSOVSQWKEKRYLQSRVOLSWOEPHPNGVIT 474
DB 443 IEAVNGVSDLSRQRYVSVNVTNNQAAPSPTVNNKKGKIAKXISLSWQEPDRPNGIIL 502
QY 475 EYEIKYEEKDQERETSTLKTSTASINNLKGTYYVQIARVTAAGYNGVSPRLDVAT 534
DB 503 EYEIKYEEKDQ-ETSTYTIKSKETITLTAEGLKASVYVQIARVTAAGYNGVSPRLDVAT 534
QY 535 LEBASGMFEAT---AVSEQNPVITIAVAVAGTIIIVFVWGFIIGRRHCGSKADQGDDE-LYFH 539
DB 559 -----FETTVSVASANDQSQIPVIAVSVTWG-VILLAVIGVLISGRRCYSKAKOLPEEKMHFH 532
QY 582 -----HCGYSKADQGDDE-LYFHSVLNHLV 609
DB 610 SSLCAVAHPSLIMRCGYSKADQPEEKMHFH---NGHIKL 647

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RESULT 9
US-10-412-277-7
; Sequence 7, Application US/10412277
; Publication No. US200301075791A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001067DIV
; CURRENT APPLICATION NUMBER: US/10/412, 277
; CURRENT FILING DATE: 2003-04-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Human
US-10-412-277-7

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Query Match 56.5%; Score 1832.5; DB 14; Length 953;
Best Local Similarity 58.2%; Pred. No. 4e-136;
Matches 340; Conservative 96; Mismatches 125; Indels 23; Gaps 7;

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QY 30 AKVLLDLSKAQOTLEWISSPPSGWEETSGIDENYTPRTTYQVCVNEPNONNMLRTNWSKGNAGRI FVELKTTLRDONS LFG 149
DB 1 SNEVNLDBSRITWGLGWIAPFKNGWEETSGIDENYAPHTHYQVCKMEONNNMLTSMISNEGASRI FIELKFTLRDONS LFG 120
QY 90 ISKGNAGRI FVELKFTLRDONS LFG 149
DB 61 ISNEGASRI FIELKFTLRDONS LFG 120
QY 150 ADESEFTQGLGERKKKLNTEVREI GPLSKGFFYLAFOVAGACIALVSVKYYKKCWTIV 209
DB 121 ADESEFTQGLGERKKKLNTEVREI GPLSKGFFYLAFOVAGACIALVSVKYYKKCWTIV 209
QY 210 ENLAVFPDVTGSESSSLVEVAGTCVSSAEBEASNSPRMHCASAGEMLVPIGKICIKAGY 269
DB 181 RHLAVFPDVTGSESSSLVEVAGTCVSSAEBEASNSPRMHCASAGEMLVPIGKICIKAGY 269
QY 270 QOKGDTCEPCGRFRFYKSSSDQLQCSRCPHSHYTHEASTCVCEKDYFRKSDPTVMACTRPPAPRAISNVNSETSFLFWIP 382
DB 239 EBNKGTQVCRPFFKASPHIQSCGKCPHSHYTHEASTCVCEKDYFRKSDPTVMACTRPPAPRAISNVNSETSFLFWIP 382
QY 330 RPPSAPQULININQTYSLFMSPPANDGENDVYRILCRCSWEOGECVPCSGNIGMPQOTGLBNDYTVMDLLAHANYTEE 414

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Db      299 RPPAPRAVAISNVNMTSVLEEMIPPADTQGRKDVSYIACKCKNSHAGVCECGHAYXL 358
Qy      390 PQQGLENTYTMWDLAHANTYFEVAVNGVSDLSRQRLPAVASITTGQAASQVSGV 449
Db      359 PROGLKNTSYVMWDLAHTYFEIEAVNGVSDLSRQRYVSNVNTTNOAASPVNTV 418
Qy      450 MKEVLORSVOLSWOEPEHPNGVITEYIKYKEDQQRRTYSTKTSTASINNLKPGT 509
Db      419 KKGIAKNSISLSMOEPRPNGIILEYIKFPEKQO-ETSYTIKSKETTTIAGELKAS 477
Qy      510 VYVEQIRAVTAAGYGNVSPRLDVAITLEBASGKMEAT---AVSSQONPVIITIAVAVAGT 566
Db      478 VYVFOIRARTAGYGVFSRFE-----FETTVFAASSDQSQIPVIASVTVG- 525
Qy      567 IILVPMVFGIIRRHGCGSKADQEGDEE-LYFHSLVNHLV 609
Db      526 VILLAVIIVGLSGRCGYSKAKODPEEKKMFH---NGHIKL 565

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RESULT 10

```

US-10-732-923-13667
; Sequence 13667, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13667
; LENGTH: 991
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-732-923-13667

```

Query Match 56.4%; Score 1829; DB 17; Length 991;

Best Local Similarity 57.4%; Pred. No. 7.9e-136;

Matches 348; Conservative 96; Mismatches 136; Indels 26; Gaps 9;

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Qy      8 PSW---IILCYIMLGFHTAGTGAQAKEYLLDSKAQOTLEWISSPSCMEISGLDENV 65
Db      15 PGMTCLELCAALRSLASPG-----SEVNLDSRTVMGLGWLAIAPKMGWEIEGVDENV 69
Qy      66 TPRTYQVCVMEPNONNMRLRTNMISKGAQRIFEVLEKFTLRDCNSLPGLGTCKETENL 125
Db      70 APIHTYQVCXKMEQNONNMWLLTSMISNCGRPASFEELKFTLRDCNSLPGLGTCKETENM 129
Qy      126 YYYETDVTGNINRENLVYKIDITIAADESFTQDGERKKMLNTEVREIPLSKKGYLA 185
Db      130 YPFESDDEGDNHIRENOYIKIDITIAADESFTELDGDVMLKLNTEVADVGLTKGFIYA 189
Qy      186 FQDVGACIALVSVKYKCKWTIVENLAVPDVTGSSFSLSVEVRCVGS-SAESELEN 244
Db      190 FQDVGACIALVSRYKCPVIRNLAIRPDTITGAASSQLEVSQGVCMHVSUTDEN-- 247
Qy      245 SPRHNSAGEMLVPIGKICIKAGYQOKGDTCEPCGRFRFYKSSODLQCSRCPHSPFSDR 304
Db      248 -PKHNSAGEMLVPIGKICIKAGYEKNNTCQVCRPFKASPHSPSCSKCPHSPSYLD 306
Qy      305 EGSSRCBCEGDIYRAPSDPYVACTRPPSAPONTLEFINQTTVLSWSPPADNGGRDVT 364
Db      307 EASTSCLEBHYFPRESDPPTMACTRPPSAPASISNVNETSVELEWIPPADTGGRKDV 366
Qy      365 YRIICKRSMQEGCVPGSGNIGWBPQOTGEDNVVTMDLAAHANTYFEVAVNGVSD 424
Db      367 YRIICKRNSHSGLEACGSHRYLPQOTGLKNTSVMMWDLAHTYFEIEAVNGVSDQ 426
Qy      425 SRSORLFAAVSITTGQAAPQVSGVMKEVRLORSVOLSWOEPEHPNGVITYEIKYEKD 484

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Db      427 NPGARQFVSVVNTTNOAPSPVSSVKKGKITTKNSISLSMOEPRPNGIILEYIKYEKD 486
Qy      485 QRETYSTIKTKSASAINNLKPGTVVFOIRATAAGYGNVSPRLDVAITLEBASGKME 544
Db      487 Q-ETSYTIKSKETTTIAGELKASAVVFOIRATAAGYGVFSRFEET-----SP 537
Qy      545 ATAVERSEQNPVITIAVAVAGTIIILVPMVFGIIRRHGCGYSKADQEGDEE-LYFHSLV 603
Db      538 VLAASSDQSQIPIL-VVSVTVGIVLLAVIGFILSGRCGYSKAKODPEEKKMFH----- 592
Qy      604 NEHLV 609
Db      593 NGHIKL 598

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RESULT 11

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US-10-029-020-63
; Sequence 63, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangoli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 1005
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-029-020-63

```

Query Match 56.2%; Score 1821; DB 15; Length 1005;

Best Local Similarity 54.6%; Pred. No. 3.5e-135;

Matches 350; Conservative 97; Mismatches 138; Indels 56; Gaps 11;

```

Qy      6 RPPSMIILCY-----IWLGFHTAGTGAQAKEYLLDSKAQOTLEWISSPSPG 54
Db      25 RVPASLGGCSAPILKGPLMTCLLCAALRTLLASPSBEVNLDSRTVYLGDIQWIAFPKNG 84
Qy      55 WEESISGLDENVTPRTYQVCVMEPNONNMRLRTNMISKGAQRIFEVLEKFTLRDCNSLP 114
Db      85 WEIEGVDENVAPPIHTYQVCXKMEQNONNMWLLTSMISNCGRSRIFELKFTLRDCNSLP 144
Qy      115 VLGTCKETPNLYYYETDVTGNINRENLVYKIDITIAADESFTQDGERKKMLNTEVREI 174
Db      145 GLGTCKETPNMYYESDDEGDNHIRENOYIKIDITIAADESFTELDGDVMLKLNTEVADV 204
Qy      175 GPLSKKGYLAFOVVGACIALVSVKYKCKWTIVENLAVPDVTGSSFSLSVEVRCVGS 234
Db      205 GPLSKKGYLAFOVVGACIALVSRYKCPVIRNLAIRPDTITGAASSQLEVSQGV 264
Qy      235 VSSAEBAENSPRHNSAGEMLVPIGKICIKAGYQOKGDTCEPCGRFRFYKSSODLQCS 294

```

Db 265 VN--HSVTDPPKMHCSAEGEMLVIGKCMCKAGYEENKGTQYCRDPFKASPHSQTCS 322
Qy 295 RCPHSPDESGSSRCCEGDGYRAPSDPPYACTRPPSAPONLIFINOTVLSLEMSPP 354
Db 323 KCPHSTHBERASSTCEKDYFRRESDDPPMACTRPPSAPRNAISNVNETSVLEMIIPP 382
Qy 355 ADNGRNDVYTRILCKRCSEWEGCEVPCGSNIGYMPQOTGLEDNVYTMDLAHANYTPE 414
Db 383 ADTGCGKDVSVYILCKCKNSHAGCEGCGHVRLPQOIGLKNTSVMMADPLATNTYTFE 442
Qy 415 VEANGVSDLSRSQRLLAAVSIITGQAAAPSOYGVKMERVLQRSVOLSMOPEHPNVT 474
Db 443 IEANGVSDLSPGTRQYVSVVNTTQAAAPSPVNVKKGIAKNSISLSWOEPPRPNIGIL 502
Qy 475 EYEIKYKEDQRETYSTLTKSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVAT 534
Db 503 EYEIKYKEDQRETYSTLTKSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVAT 534
Qy 535 LEEASGMFEATAV--SSEONPVIIIAVAVAGTIIILVFMVFGFII-----GRR- 581
Db 559 -----FETTPVFGASNDOSQIPITIGSVTVGVIIILAVMI-GFLLSGSCCEGCGGRAS 609
Qy 582 -----HCGYSKADQEGDE-LYFHSLVNTNHLVS 609
Db 610 SLCAVAHPSLIWRCGYSKAKQDPBEERKMFH---NGHIKL 646

RESULT 12
US-10-316-124-3
; Sequence 3, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; FILE REFERENCE: MFI01-291P1RM
; CURRENT APPLICATION NUMBER: US/10/316,124
; PRIORITY FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIORITY FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastaSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-316-124-3

Query Match 56.1%; Score 1819; DB 14; Length 1037;
Best Local Similarity 55.1%; Pred. No. 5.3e-135;
Matches 348; Conservative 98; Mismatches 134; Indels 52; Gaps 11;
Qy 6 RFBWM--IILCYIMLGFALTGEQAQKVELLLDSKAQOTLELWISSPSPGWEHISLDE 63
Db 37 RAPIMTLLLC-----AALRTLLASPSNEVNLDSRTVMGDLGIAFPKKGWEIIGRVD 91
Qy 64 NYTPIRTYQVCOVMEPNQNNMLRTNMTSKGNAORIFVELKFTLRDQSLFGVGTCKETP 123
Db 92 NYAPIHIVQYCKWEQNNWMLTWSINEGASRIFELKFTLRDQSLFGVGTCKETP 151
Qy 124 NLVYETDYDTGRNIRENLVYKIDTIAADESFTQGDIGERRKMLNTEVRE IGPLSKKGFY 183
Db 152 NMYEESDDQNGRNIKENQYIKIDTIAADESFTLIDGDRVMKLNTEVRLVGPLSKKGFY 211
Qy 184 LAFODVACIALVSVKYYKKCWIVENLAVFPPTVYGSFSSLYVRGICVSAEEAE 243
Db 212 LAFQDVACIALVSVRYKKCBVHLLVFPPTIIGAGSSQLLEVSGCIVN--HSVTD 269
Qy 244 NSPRMHCSAEGEMLVPIGKCIKAGYQKGDTCPCGRRFPYKSSODLQCSRCPHSHSD 303
Db 270 EPRMHCSAEGEMLVPIGKCMCKAGYEENKGTQYCRDPFKASPHIQCCKGCPHSHSYH 329

Qy 304 REGSSRCCEGDGYRAPSDPPYACTRPPSAPONLIFINOTVLSLEMSPPADNGRNDV 363
Db 330 EEAOSTCVCCEKDYFRRESDDPPMACTRPPSAPRNAISNVNETSVLEMIIPADTGGRKDV 389
Qy 364 TYIILCKRCSEWEGCEVPCGSNIGYMPQOTGLEDNVYTMDLAHANYTPEVAVNGVSD 423
Db 390 SYIACKKNSHAGVEECGCGHVRLPQOIGLKNTSVMMADPLATNTYTFEIAVNGVSD 449
Qy 424 LRSORLFAVSIITGQAAAPSOYGVKMERVLQRSVOLSMOPEHPNVTYEIKYK 483
Db 450 LSPGAQYVSVNTTQAAAPSPVNVKKGIAKNSISLSWOEPPRPNIGIL 509
Qy 484 DQRETYSTLTKSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVATLEEASGMFE 543
Db 510 DQ-ETSYTIKSKETTTAEGLKPAVYVFOIRAVTAAGYNSPRLDVAT 557
Qy 544 EAT--AVSEONPVIIIAVAVAGTIIILVFMVFGFII-----GRR- 581
Db 558 ETPVFAASDQSLIVAVSVTVG-VILLAVIGVLLSGSCCEGCGGRASLCAVAHPI 616
Qy 582 ---HCGYSKADQEGDE-LYFHSLVNTNHLVS 609
Db 617 LWRGYSKAKQDPBEERKMFH---NGHIKL 644

RESULT 13
US-10-353-690-40
; Sequence 40, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Domognue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacqueline
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: Cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 11720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 58590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
; FILE REFERENCE: MFI02-018P1RNDNMIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; PRIORITY FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIORITY FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIORITY FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIORITY FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIORITY FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIORITY FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIORITY FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIORITY FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIORITY FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIORITY FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIORITY FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 1037
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-353-690-40

Query Match 56.1%; Score 1819; DB 15; Length 1037;
Best Local Similarity 55.1%; Pred. No. 5,3e-135;
Matches 348; Conservative 98; Mismatches 134; Indels 52; Gaps 11;

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QY 6 RPSW-IIIICYMLGFAHGEAQAKEYLLDSKAQOTLEWISSPPSGMEISGIDE 63
D 37 RAPLMTCLLC-----AALRTLLASPSNEVNLDSRTVMGDLGWIAPKMGMEIEGYDE 91
QY 64 NYTPIRTYQCVQWEPNQNMLRTNWSKGAQRIFVELKFTLDCNSLPGLGCKETF 123
D 92 NYAIIHTYQCKWEQNNMNLTSWISNEGASRIFFELKFTLDCNSLPGLGCKETF 151
QY 124 NLVYETDYDGRNIRENLVYKIDTIADESFTQDLGERRMKLTVEIREIGPLSKGFY 183
D 152 NMYEFESDDQGRNIRENOYIKIDTIADESFTLDCRMKLTVEIRDYGLSKGFY 211
QY 184 LAFQDVACIALVSVKYKKCWITVENLAVFPPTVTGSEFSSLYVRGTCVSSAEEBAE 243
D 212 LAFQDVACIALVSVKYKKCPVVRHLAVFPPTITGADSSQLLEVSGSCVN--HSVTD 269
QY 244 NSPRMHSAGEMLVPIGKCIKAGYQOKGDTCEPCGRPFYKSSSODLQCSRCPHSPSD 303
D 270 EPPMHSAGEMLVPIGKCMCKAGYEEKGTCCVCRPGFFKASPHIOSCGKCPHSTYH 329
QY 304 REGSRCECEDGYRAPSDPYVACTRPPSAPOMLIFINOTVLSLEWSPPADNGRNDV 363
D 330 EEAISTCVCEDYRRRSDPYVACTRPPSAPRAISVNETSVFLEWIPPADTGRKDV 389
QY 364 TYRILCRCSWEGECVPCGSNIGYPOQTLSDNYVTMDLLAHANTFEVAVNGYSD 423
D 390 SYTIACKCKNSHACVCECGHVRYLPRQSLKNTSVMMVDLLAHNTYFIEIENVGSD 449
QY 424 LSRQRLFAAVSITTGQAAPSOVSGWKKERYLORSVOLSMOEPHPNVCITVEYEIKYK 483
D 450 LSPBARQVSVNVTNQAAPSPVTVNKKGLAKNSISLSMOEPHPNIIILEYEIKHEK 509
QY 484 DQERTYSTLTKSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVATLEASGMF 543
D 510 DQ-ETSTYTIKSKETITTAELKPAASYVFOIRARTAGYGVFSRRE-----F 557
QY 544 EAT---AVSSQNVIILAVAVAGTIIIVPMVFGFI-----GRR----- 581
D 558 ETTVFPAASDQSQIPVIAVSVTG-VILLAVIGVLLSGSCCGCGRASLCAVAHPI 616
QY 582 ---HGYSKADQEGDE-LYFHSLVTHNSLV 609
D 617 LIWRGYSKAKQDPEEKMHFH---NGHIDL 644
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RESULT 14
US-11-064-551-3
Sequence 3, Application US/11064551
Publication No. US20050142604A1
GENERAL INFORMATION:
APPLICANT: Logan, Thomas Joseph
APPLICANT: Chun, Miyoung
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
FILE REFERENCE: MP01-291PIRM
CURRENT APPLICATION NUMBER: US/11/064,551
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: 60/339,995
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3

LENGTH: 1037
TYPE: PRT
ORGANISM: Homo sapiens
US-11-064-551-3

Query Match 56.1%; Score 1819; DB 20; Length 1037;
Best Local Similarity 55.1%; Pred. No. 5,3e-135;
Matches 348; Conservative 98; Mismatches 134; Indels 52; Gaps 11;

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QY 6 RPSW-IIIICYMLGFAHGEAQAKEYLLDSKAQOTLEWISSPPSGMEISGIDE 63
D 37 RAPLMTCLLC-----AALRTLLASPSNEVNLDSRTVMGDLGWIAPKMGMEIEGYDE 91
QY 64 NYTPIRTYQCVQWEPNQNMLRTNWSKGAQRIFVELKFTLDCNSLPGLGCKETF 123
D 92 NYAIIHTYQCKWEQNNMNLTSWISNEGASRIFFELKFTLDCNSLPGLGCKETF 151
QY 124 NLVYETDYDGRNIRENLVYKIDTIADESFTQDLGERRMKLTVEIREIGPLSKGFY 183
D 152 NMYEFESDDQGRNIRENOYIKIDTIADESFTLDCRMKLTVEIRDYGLSKGFY 211
QY 184 LAFQDVACIALVSVKYKKCWITVENLAVFPPTVTGSEFSSLYVRGTCVSSAEEBAE 243
D 212 LAFQDVACIALVSVKYKKCPVVRHLAVFPPTITGADSSQLLEVSGSCVN--HSVTD 269
QY 244 NSPRMHSAGEMLVPIGKCIKAGYQOKGDTCEPCGRPFYKSSSODLQCSRCPHSPSD 303
D 270 EPPMHSAGEMLVPIGKCMCKAGYEEKGTCCVCRPGFFKASPHIOSCGKCPHSTYH 329
QY 304 REGSRCECEDGYRAPSDPYVACTRPPSAPOMLIFINOTVLSLEWSPPADNGRNDV 363
D 330 EEAISTCVCEDYRRRSDPYVACTRPPSAPRAISVNETSVFLEWIPPADTGRKDV 389
QY 364 TYRILCRCSWEGECVPCGSNIGYPOQTLSDNYVTMDLLAHANTFEVAVNGYSD 423
D 390 SYTIACKCKNSHACVCECGHVRYLPRQSLKNTSVMMVDLLAHNTYFIEIENVGSD 449
QY 424 LSRQRLFAAVSITTGQAAPSOVSGWKKERYLORSVOLSMOEPHPNVCITVEYEIKYK 483
D 450 LSPBARQVSVNVTNQAAPSPVTVNKKGLAKNSISLSMOEPHPNIIILEYEIKHEK 509
QY 484 DQERTYSTLTKSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVATLEASGMF 543
D 510 DQ-ETSTYTIKSKETITTAELKPAASYVFOIRARTAGYGVFSRRE-----F 557
QY 544 EAT---AVSSQNVIILAVAVAGTIIIVPMVFGFI-----GRR----- 581
D 558 ETTVFPAASDQSQIPVIAVSVTG-VILLAVIGVLLSGSCCGCGRASLCAVAHPI 616
QY 582 ---HGYSKADQEGDE-LYFHSLVTHNSLV 609
D 617 LIWRGYSKAKQDPEEKMHFH---NGHIDL 644
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RESULT 15
US-10-412-277-8
Sequence 8, Application US/10412277
Publication No. US20030175791A1
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: C1001067D1V
CURRENT APPLICATION NUMBER: US/10/412,277
CURRENT FILING DATE: 2003-04-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 975
TYPE: PRT
ORGANISM: Human
US-10-412-277-8

Query Match	55.8%;	Score 1808.5;	DB 14;	Length 975;
Best Local Similarity	56.3%;	Pred. No. 3.3e-134;		
Matches 341;	Conservative 96;	Mismatches 124;	Indels 45;	Gaps 9;

[illegible]

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Search completed: August 23, 2005, 08:56:30
Job time : 113.063 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 21.2217 Seconds
(without alignments)
2145.727 Million cell updates/sec

Title: US-10-073-064-3
3243
Sequence: 1 MVQTRPPSWILCYMLG.....EGDELYFSLVNEHLSVL 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3243	100.0	610	3	US-08-368-776A-3
2	3243	100.0	610	5	PCT-US96-00419-3
3	3199	98.6	626	3	US-08-368-776A-5
4	3199	98.6	626	5	PCT-US96-00419-5
5	3192	98.4	994	3	US-08-368-776A-12
6	3191	98.4	998	3	US-08-368-776A-2
7	3191	98.4	998	5	PCT-US96-00419-2
8	3151.5	97.2	993	3	US-08-368-776A-11
9	3139	96.8	998	2	US-08-449-645A-17
10	3139	96.8	998	2	US-08-702-367A-17
11	3139	96.8	998	4	US-09-949-016-6501
12	3139	96.8	998	5	PCT-US95-04681-17
13	3139	96.8	1005	4	US-09-949-016-9901
14	1843	56.8	991	2	US-08-449-645A-13
15	1843	56.8	991	2	US-08-702-367A-13
16	1843	56.8	991	5	PCT-US95-04681-13
17	1835.5	56.6	967	2	US-08-449-645A-30
18	1835.5	56.6	967	2	US-08-702-367A-30
19	1832.5	56.5	953	4	US-09-751-389-7
20	1824	56.2	1005	2	US-08-469-537A-103
21	1808.5	55.8	975	1	US-09-751-389-8
22	1793	55.3	983	4	US-08-167-919A-10
23	1793	55.3	983	2	US-08-449-645A-21
24	1793	55.3	983	2	US-08-702-367A-21
25	1793	55.3	983	3	US-08-715-106-10
26	1793	55.3	983	4	US-09-442-649-10
27	1793	55.3	983	5	PCT-US95-04681-21

28	1786.5	55.1	968	4	US-09-751-389-6	Sequence 6, Appli
29	1778.5	54.8	983	1	US-08-162-809-16	Sequence 16, Appli
30	1777	54.8	982	2	US-08-673-789-4	Sequence 4, Appli
31	1736.5	53.5	986	2	US-08-449-645A-15	Sequence 15, Appli
32	1736.5	53.5	986	2	US-08-702-367A-15	Sequence 15, Appli
33	1736.5	53.5	986	5	PCT-US95-04681-15	Sequence 15, Appli
34	1736.5	53.5	997	4	US-09-949-016-7171	Sequence 36, Appli
35	1729.5	53.3	1104	4	US-08-222-616-16	Sequence 36, Appli
36	1729.5	53.3	1104	3	US-08-446-648-36	Sequence 36, Appli
37	1729.5	53.3	1104	4	US-09-982-610-16	Sequence 36, Appli
38	1729.5	53.3	1104	5	PCT-US95-04228-36	Sequence 36, Appli
39	1729	53.3	986	2	US-08-673-789-3	Sequence 36, Appli
40	1701.5	52.5	1005	4	US-09-949-016-6968	Sequence 6968, Ap
41	1701.5	52.5	1005	4	US-09-949-016-10620	Sequence 10620, A
42	1670.5	51.5	1036	4	US-09-751-389-2	Sequence 2, Appli
43	1666.5	51.4	942	4	US-10-004-542-2	Sequence 2, Appli
44	1666.5	51.4	942	4	US-10-430-797-2	Sequence 2, Appli
45	1662	51.2	948	2	US-08-469-537A-101	Sequence 101, App

ALIGNMENTS

RESULT 1
US-08-368-776A-3
Sequence 3, Application US/08368776A
Patent No. 6300482
GENERAL INFORMATION:
APPLICANT: Closssek, Thomas
APPLICANT: Ullrich, Axel
APPLICANT: Millauret, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF MDK1
TITLE OF INVENTION: SIGNAL TRANSDUCTION
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Filth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368, 776A
FILING DATE: January 3, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

none

MOLECULE TYPE: peptide
US-08-368-776A-3

Query Match 100.0%; Score 3243; DB 3; Length 610;
Best Local Similarity 100.0%; Pred. No. 4.7e-294;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVTQTRPPSWIILCYIMLGFPAHTGEAQAKEYLLDSKAQOTELEWISSPPSGMEIISG 60
DB 1 MVTQTRPPSWIILCYIMLGFPAHTGEAQAKEYLLDSKAQOTELEWISSPPSGMEIISG 60
QY 61 LDENVTPRTYQVCQWEPNOMNMLRTNWSKGAORIFVELKFTLRDNCSLPGVLTGCK 120
DB 61 LDENVTPRTYQVCQWEPNOMNMLRTNWSKGAORIFVELKFTLRDNCSLPGVLTGCK 120
QY 121 EFTNLYYEEDYDYGNIHRENLVYKIDTIAADESFTQDGLGERKMLNTEVREIGPLSKK 180
DB 121 EFTNLYYEEDYDYGNIHRENLVYKIDTIAADESFTQDGLGERKMLNTEVREIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWITIYENLAVFPDVTGSEFSSLVEVAGTCVSSAEE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWITIYENLAVFPDVTGSEFSSLVEVAGTCVSSAEE 240
QY 241 EAENSPRMHCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRRFYKSSSODLQCSRCPHIS 300
DB 241 EAENSPRMHCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRRFYKSSSODLQCSRCPHIS 300
QY 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPSAPONLIENINQTVLSLEWSPADNGGR 360
DB 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPSAPONLIENINQTVLSLEWSPADNGGR 360
QY 361 NDVTYRILCKRCGMEGECVPCGSNIGYMPQGTGLENDYVTVMDLLAHANYTFEVAVNG 420
DB 361 NDVTYRILCKRCGMEGECVPCGSNIGYMPQGTGLENDYVTVMDLLAHANYTFEVAVNG 420
QY 421 VSDLSRSORLFAVSIITGQAAPSOVSGWKEKERVLSQWQEPHHPGVITTEYIKY 480
DB 421 VSDLSRSORLFAVSIITGQAAPSOVSGWKEKERVLSQWQEPHHPGVITTEYIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVALTEBASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVALTEBASG 540
QY 541 KMFEATAVSSQNPVITIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADCEGBELYFHS 600
DB 541 KMFEATAVSSQNPVITIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADCEGBELYFHS 600
QY 601 LVTNEHLSVL 610
DB 601 LVTNEHLSVL 610

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RESULT 2 PCT-US96-00419-3

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; Sequence 3, Application PC/TUS9600419
; GENERAL INFORMATION:
; APPLICANT: Thomas Closek, Axel Ulirich, Birgit
; APPLICANT: Millaue
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00419
; FILING DATE: January 3, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: none
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-00419-3

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Query Match 100.0%; Score 3243; DB 5; Length 610;
Best Local Similarity 100.0%; Pred. No. 4.7e-294;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVTQTRPPSWIILCYIMLGFPAHTGEAQAKEYLLDSKAQOTELEWISSPPSGMEIISG 60
DB 1 MVTQTRPPSWIILCYIMLGFPAHTGEAQAKEYLLDSKAQOTELEWISSPPSGMEIISG 60
QY 61 LDENVTPRTYQVCQWEPNOMNMLRTNWSKGAORIFVELKFTLRDNCSLPGVLTGCK 120
DB 61 LDENVTPRTYQVCQWEPNOMNMLRTNWSKGAORIFVELKFTLRDNCSLPGVLTGCK 120
QY 121 EFTNLYYEEDYDYGNIHRENLVYKIDTIAADESFTQDGLGERKMLNTEVREIGPLSKK 180
DB 121 EFTNLYYEEDYDYGNIHRENLVYKIDTIAADESFTQDGLGERKMLNTEVREIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWITIYENLAVFPDVTGSEFSSLVEVAGTCVSSAEE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWITIYENLAVFPDVTGSEFSSLVEVAGTCVSSAEE 240
QY 241 EAENSPRMHCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRRFYKSSSODLQCSRCPHIS 300
DB 241 EAENSPRMHCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRRFYKSSSODLQCSRCPHIS 300
QY 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPSAPONLIENINQTVLSLEWSPADNGGR 360
DB 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPSAPONLIENINQTVLSLEWSPADNGGR 360
QY 361 NDVTYRILCKRCGMEGECVPCGSNIGYMPQGTGLENDYVTVMDLLAHANYTFEVAVNG 420
DB 361 NDVTYRILCKRCGMEGECVPCGSNIGYMPQGTGLENDYVTVMDLLAHANYTFEVAVNG 420
QY 421 VSDLSRSORLFAVSIITGQAAPSOVSGWKEKERVLSQWQEPHHPGVITTEYIKY 480
DB 421 VSDLSRSORLFAVSIITGQAAPSOVSGWKEKERVLSQWQEPHHPGVITTEYIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVALTEBASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVALTEBASG 540
QY 541 KMFEATAVSSQNPVITIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADCEGBELYFHS 600
DB 541 KMFEATAVSSQNPVITIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADCEGBELYFHS 600
QY 601 LVTNEHLSVL 610
DB 601 LVTNEHLSVL 610

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RESULT 3

US-08-368-776A-5

Sequence 5, Application US/08368776A
Patent No. 630482

GENERAL INFORMATION:

APPLICANT: Ciosek, Thomas

APPLICANT: Ullrich, Axel

APPLICANT: Millaer, Birgit

TITLE OF INVENTION: METHODS FOR DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF MDX1

TITLE OF INVENTION: SIGNAL TRANSDUCTION

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Lyon & Lyon Street

STREET: 633 West Filth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/368,776A

FILING DATE: January 3, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below: none

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 626 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-368-776A-5

Query Match

Best Local Similarity 98.6%; Score 3199; DB 3; Length 626;

Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVOGTRPSPWILLCYIWLGFAGTGEAQAQAVILLDSKAQOTELWISSPPSGMBEISG 60

DB 1 MVOGTRPSPWILLCYIWLGFAGTGEAQAQAVILLDSKAQOTELWISSPPSGMBEISG 60

QY 61 LDENVTPRTYOVQWEPNOMNMLRTWISKNAQRIFVFLKFTLRDNCNLPGLGTCK 120

DB 61 LDENVTPRTYOVQWEPNOMNMLRTWISKNAQRIFVFLKFTLRDNCNLPGLGTCK 120

QY 121 ETPNLYYETDYDGRNIRENLYVYKIDTIADDESFTQDGLGRKKKNTVEIRIGPLSKK 180

DB 121 ETPNLYYETDYDGRNIRENLYVYKIDTIADDESFTQDGLGRKKKNTVEIRIGPLSKK 180

QY 121 ETPNLYYETDYDGRNIRENLYVYKIDTIADDESFTQDGLGRKKKNTVEIRIGPLSKK 180

DB 121 ETPNLYYETDYDGRNIRENLYVYKIDTIADDESFTQDGLGRKKKNTVEIRIGPLSKK 180

QY 181 GFYLAFOVGAACIALVSVKYYKKCWITVENLAVFPDPTVTGSSEFSLVEVRGTCVSSAEE 240

DB 181 GFYLAFOVGAACIALVSVKYYKKCWITVENLAVFPDPTVTGSSEFSLVEVRGTCVSSAEE 240

QY 181 GFYLAFOVGAACIALVSVKYYKKCWITVENLAVFPDPTVTGSSEFSLVEVRGTCVSSAEE 240

DB 181 GFYLAFOVGAACIALVSVKYYKKCWITVENLAVFPDPTVTGSSEFSLVEVRGTCVSSAEE 240

QY 181 GFYLAFOVGAACIALVSVKYYKKCWITVENLAVFPDPTVTGSSEFSLVEVRGTCVSSAEE 240

DB 181 GFYLAFOVGAACIALVSVKYYKKCWITVENLAVFPDPTVTGSSEFSLVEVRGTCVSSAEE 240

QY 181 GFYLAFOVGAACIALVSVKYYKKCWITVENLAVFPDPTVTGSSEFSLVEVRGTCVSSAEE 240

DB 181 GFYLAFOVGAACIALVSVKYYKKCWITVENLAVFPDPTVTGSSEFSLVEVRGTCVSSAEE 240

DB 181 GFYLAFOVGAACIALVSVKYYKKCWITVENLAVFPDPTVTGSSEFSLVEVRGTCVSSAEE 240

QY 241 EAENSPPMHCSABEGEWLPIGKCIKAGYQOKGDTCEPCGRPFYKSSODLQCSRCPHHS 300

DB 241 EAENSPPMHCSABEGEWLPIGKCIKAGYQOKGDTCEPCGRPFYKSSODLQCSRCPHHS 300

QY 301 FSDREGSSRCCEBDGYRAPSDPEYACTRPPSAQMLININOTVLSLEWSPADNGR 360

DB 301 FSDREGSSRCCEBDGYRAPSDPEYACTRPPSAQMLININOTVLSLEWSPADNGR 360

QY 361 NDVYRILRCRCSMEQECVPCSGNIGYMPQGTLENNYVMDLLAHANTFEVEAVNG 420

DB 361 NDVYRILRCRCSMEQECVPCSGNIGYMPQGTLENNYVMDLLAHANTFEVEAVNG 420

QY 421 VSDLSRQRLFAAVSITGGAAPSOVSGWKKERYLORSVOLSMOEPHPNGVITEYEIKY 480

DB 421 VSDLSRQRLFAAVSITGGAAPSOVSGWKKERYLORSVOLSMOEPHPNGVITEYEIKY 480

QY 481 YEKQRERTYSTLKSTKSASINNLKPGTYVFOIRAVTAAGYGNYSPLDVATLEBASG 540

DB 481 YEKQRERTYSTLKSTKSASINNLKPGTYVFOIRAVTAAGYGNYSPLDVATLEBASG 540

QY 541 KMFATVSSSEONPVIIIAVAVAGTIIIVPMVGFIIGRHCGYSKADQGBDELYFHS 600

DB 541 KMFATVSSSEONPVIIIAVAVAGTIIIVPMVGFIIGRHCGYSKADQGBDELYFHS 600

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

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DB 601 L 601

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DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

QY 601 L 601

DB 601 L 601

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-00419-5

Query Match 98.6%; Score 3199; DB 5; Length 624;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVOVTRPSPWIIICYIMLGFATGGAQAKEVLLDSKAQOTLELMISSPPSGMEIISG 60
DB 1 MVOVTRPSPWIIICYIMLGFATGGAQAKEVLLDSKAQOTLELMISSPPSGMEIISG 60
QY 61 LDENVYPIRTYQVCQVMEPNQNMMLRTNWSKNAQRIFEVLEKFTLDCNSLPGVLGTCK 120
DB 61 LDENVYPIRTYQVCQVMEPNQNMMLRTNWSKNAQRIFEVLEKFTLDCNSLPGVLGTCK 120
QY 121 ETEFLYYEEDYDYGNNIRENLVYKIDTIAADESFTQDGERKMLNTEVREIGPLSKK 180
DB 121 ETEFLYYEEDYDYGNNIRENLVYKIDTIAADESFTQDGERKMLNTEVREIGPLSKK 180
QY 181 GFYIAFQDVGACIALVSVKYKKWTVIENLAVFPDVTGSEFSSLVEVREGTGVSSAEE 240
DB 181 GFYIAFQDVGACIALVSVKYKKWTVIENLAVFPDVTGSEFSSLVEVREGTGVSSAEE 240
QY 241 EAENSPPMHCSAEGEWLVPIGKCIKAGYQKGDTCPCGRRFYKSSODLQCSRPTHS 300
DB 241 EAENSPPMHCSAEGEWLVPIGKCIKAGYQKGDTCPCGRRFYKSSODLQCSRPTHS 300
QY 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFINQTVSLTWSPPADNGGR 360
DB 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFINQTVSLTWSPPADNGGR 360
QY 361 NDVTYRILCKRCSEWGECEVPCGSGNIGMPQOTGLENNYTVMDLAAHYTFPEVAVNG 420
DB 361 NDVTYRILCKRCSEWGECEVPCGSGNIGMPQOTGLENNYTVMDLAAHYTFPEVAVNG 420
QY 421 VSDLSRQRLFAAVSITTTGAAPSQVSGVWKERVLSVOLSWQEPHNPVITTEYIKY 480
DB 421 VSDLSRQRLFAAVSITTTGAAPSQVSGVWKERVLSVOLSWQEPHNPVITTEYIKY 480
QY 481 YEKQREERTYSTLKTSTASINNLKPGTYVYFOIRAVTAAGYGNYSBPRIDVATLEBASG 540
DB 481 YEKQREERTYSTLKTSTASINNLKPGTYVYFOIRAVTAAGYGNYSBPRIDVATLEBASG 540
QY 541 KMFPAATVSSQONVITIAVAVAGTIIIVMVGFTIIGRRHCGYSKADQEGDELYFHS 600
DB 541 KMFPAATVSSQONVITIAVAVAGTIIIVMVGFTIIGRRHCGYSKADQEGDELYFHS 600
QY 601 L 601
DB 601 L 601

RESULT 5
US-08-368-776A-12
Sequence 12, Application US/08368776A
Patent No. 6300482

GENERAL INFORMATION:
APPLICANT: Ciosek, Thomas
APPLICANT: Ullrich, Axel
APPLICANT: Millauer, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF MDK1
TITLE OF INVENTION: SIGNAL TRANSDUCTION
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California

COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,776A
FILING DATE: January 3, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-368-776A-12

Query Match 98.4%; Score 3192; DB 3; Length 994;
Best Local Similarity 99.5%; Pred. No. 5.9e-289;
Matches 600; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVOVTRPSPWIIICYIMLGFATGGAQAKEVLLDSKAQOTLELMISSPPSGMEIISG 60
DB 1 MVOVTRPSPWIIICYIMLGFATGGAQAKEVLLDSKAQOTLELMISSPPSGMEIISG 60
QY 61 LDENVYPIRTYQVCQVMEPNQNMMLRTNWSKNAQRIFEVLEKFTLDCNSLPGVLGTCK 120
DB 61 LDENVYPIRTYQVCQVMEPNQNMMLRTNWSKNAQRIFEVLEKFTLDCNSLPGVLGTCK 120
QY 121 ETEFLYYEEDYDYGNNIRENLVYKIDTIAADESFTQDGERKMLNTEVREIGPLSKK 180
DB 121 ETEFLYYEEDYDYGNNIRENLVYKIDTIAADESFTQDGERKMLNTEVREIGPLSKK 180
QY 181 GFYIAFQDVGACIALVSVKYKKWTVIENLAVFPDVTGSEFSSLVEVREGTGVSSAEE 240
DB 181 GFYIAFQDVGACIALVSVKYKKWTVIENLAVFPDVTGSEFSSLVEVREGTGVSSAEE 240
QY 241 EAENSPPMHCSAEGEWLVPIGKCIKAGYQKGDTCPCGRRFYKSSODLQCSRPTHS 300
DB 241 EAENSPPMHCSAEGEWLVPIGKCIKAGYQKGDTCPCGRRFYKSSODLQCSRPTHS 300
QY 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFINQTVSLTWSPPADNGGR 360
DB 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFINQTVSLTWSPPADNGGR 360
QY 361 NDVTYRILCKRCSEWGECEVPCGSGNIGMPQOTGLENNYTVMDLAAHYTFPEVAVNG 420
DB 361 NDVTYRILCKRCSEWGECEVPCGSGNIGMPQOTGLENNYTVMDLAAHYTFPEVAVNG 420
QY 421 VSDLSRQRLFAAVSITTTGAAPSQVSGVWKERVLSVOLSWQEPHNPVITTEYIKY 480
DB 421 VSDLSRQRLFAAVSITTTGAAPSQVSGVWKERVLSVOLSWQEPHNPVITTEYIKY 480
QY 481 YEKQREERTYSTLKTSTASINNLKPGTYVYFOIRAVTAAGYGNYSBPRIDVATLEBASG 540
DB 481 YEKQREERTYSTLKTSTASINNLKPGTYVYFOIRAVTAAGYGNYSBPRIDVATLEBASG 540

Qy 541 KMFATAVSSSEONVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGBDELYFHS 600
Db 541 KMFATAVSSSEONVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGBDELYFHS 600

Qy 601 LVT 603
Db 601 TKT 603

RESULT 6
US-08-368-776A-2
Sequence 2, Application US/08368776A
Patent No. 6300482

GENERAL INFORMATION:
APPLICANT: Cioseck, Thomas
APPLICANT: Ulrich, Axel
APPLICANT: Millaue, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF MDK1
TITLE OF INVENTION: SIGNAL TRANSDUCTION
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368, 776A
FILING DATE: January 3, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: none
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-368-776A-2

Query Match 98.4%; Score 3191; DB 3; Length 998;
Best Local Similarity 100.0%; Pred. No. 7,4e-289;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVTGTRPSPWIIICVIMLGFAGTGEAQAKEVLLDSKAQOTLEWISSPPSGWEIISG 60
Db 1 MVTGTRPSPWIIICVIMLGFAGTGEAQAKEVLLDSKAQOTLEWISSPPSGWEIISG 60
Qy 61 LDENVYPIRYOVQVMEPNONMRLTNWISKGAORI FVELKFTLRDCNSLPVGLGTCK 120
Db 61 LDENVYPIRYOVQVMEPNONMRLTNWISKGAORI FVELKFTLRDCNSLPVGLGTCK 120

Db 61 LDENVYPIRYOVQVMEPNONMRLTNWISKGAORI FVELKFTLRDCNSLPVGLGTCK 120
Qy 121 ETFNLVYETEDYDPTGRNIRENLVYKIDITIADESEFTQDGLGERMKLNTREIRIGPSKK 180
Db 121 ETFNLVYETEDYDPTGRNIRENLVYKIDITIADESEFTQDGLGERMKLNTREIRIGPSKK 180
Qy 181 GFYLAPODVGACIALVSKYKYKWCMTIVENLAVFPDVTGSEFSSLVEVAGTCVSSAEE 240
Db 181 GFYLAPODVGACIALVSKYKYKWCMTIVENLAVFPDVTGSEFSSLVEVAGTCVSSAEE 240
Qy 241 EAENSPRMHCSABEEMLVPIGKCI CKAGYQOKGTCPCGRRFPYKSSSODLQCRCTHS 300
Db 241 EAENSPRMHCSABEEMLVPIGKCI CKAGYQOKGTCPCGRRFPYKSSSODLQCRCTHS 300
Qy 301 FSDRESSRCCEDEGYRAPSDPPYVACTPPSAPOULIFININTVLSLESPPADNGR 360
Db 301 FSDRESSRCCEDEGYRAPSDPPYVACTPPSAPOULIFININTVLSLESPPADNGR 360
Qy 361 NDVYRIILCKRCSEWQECVPCGSNIGMPQOTGLEBNVYVMDLAAHANYTFEVAANG 420
Db 361 NDVYRIILCKRCSEWQECVPCGSNIGMPQOTGLEBNVYVMDLAAHANYTFEVAANG 420
Qy 421 VSDLSRQRLFAVSIITGQAAPQSVGVKMERVLQSRVLSWQEPHPNGVITEYIKY 480
Db 421 VSDLSRQRLFAVSIITGQAAPQSVGVKMERVLQSRVLSWQEPHPNGVITEYIKY 480
Qy 481 YEKQRERTYTLTKTSTASINNLKPGTYVFOIRAVTAAGVNSPRLDVATLEASG 540
Db 481 YEKQRERTYTLTKTSTASINNLKPGTYVFOIRAVTAAGVNSPRLDVATLEASG 540
Qy 541 KMFATAVSSSEONVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGBDELYFHS 599
Db 541 KMFATAVSSSEONVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGBDELYFHS 599

RESULT 7
PCT-US96-00419-2
Sequence 2, Application PC/TUS9600419
GENERAL INFORMATION:

APPLICANT: Thomas Cioseck, Axel Ulrich, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00419
FILING DATE: January 3, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: none
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 998
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US96-00419-2

Query Match 98.4%; Score 3191; DB 5; Length 998;
 Best Local Similarity 100.0%; Pred. No. 7,4e-289;
 Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVOQTRPSPWIIICYYIMLGFATGGAQAQAEVLLDLSKAQOTELMISPPSGMEISG 60
 DB 1 MVOQTRPSPWIIICYYIMLGFATGGAQAQAEVLLDLSKAQOTELMISPPSGMEISG 60
 QY 61 LDENVTPIRITYQVQVMEPNQNNMLRTNWSKNAQRIPELKTLLADCNLPGVIGTCK 120
 DB 61 LDENVTPIRITYQVQVMEPNQNNMLRTNWSKNAQRIPELKTLLADCNLPGVIGTCK 120
 QY 121 ETEFLYYETDVTGKRIENLYVKIDTIAADESFTQDGERKMLNTEVREIGPLSKK 180
 DB 121 ETEFLYYETDVTGKRIENLYVKIDTIAADESFTQDGERKMLNTEVREIGPLSKK 180
 QY 181 GFYLAFQDVACIALSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVIGTCVSSABE 240
 DB 181 GFYLAFQDVACIALSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVIGTCVSSABE 240
 QY 241 EAENSPPMHCSAEGEMLVPIGKICIKAGYQOKGDTCEPGRRFPKSSSDOLQSCRPTHS 300
 DB 241 EAENSPPMHCSAEGEMLVPIGKICIKAGYQOKGDTCEPGRRFPKSSSDOLQSCRPTHS 300
 QY 301 FSDREGSSRCECEDGYRAPSDDPPYACTRPPSAPQNLFININQTVLSLESPPADNGR 360
 DB 301 FSDREGSSRCECEDGYRAPSDDPPYACTRPPSAPQNLFININQTVLSLESPPADNGR 360
 QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTVMDLLAHANFTVEEAVNG 420
 DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTVMDLLAHANFTVEEAVNG 420
 QY 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGWKEKERVLSVOLSWQEPBHPN3VITEYEIKY 480
 DB 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGWKEKERVLSVOLSWQEPBHPN3VITEYEIKY 480
 QY 481 YEKQQRERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSPPRLDVATLEBASG 540
 DB 481 YEKQQRERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSPPRLDVATLEBASG 540
 QY 541 KMFEBATVSSQNEPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDELYFH 599
 DB 541 KMFEBATVSSQNEPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDELYFH 599

RESULT 8
 US-08-368-776A-11
 Sequence 11, Application US/08368776A
 Patent No. 6300482

GENERAL INFORMATION:
 APPLICANT: Ciosesek, Thomas
 APPLICANT: Ulrich, Axel
 APPLICANT: Millauer, Birgit
 TITLE OF INVENTION: METHODS FOR DIAGNOSIS
 TITLE OF INVENTION: AND TREATMENT OF MDK1
 TITLE OF INVENTION: SIGNAL TRANSDUCTION
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California

COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/368,776A
 FILING DATE: January 3, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below: none
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 208/007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 993 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-368-776A-11

Query Match 97.2%; Score 3151.5; DB 3; Length 993;
 Best Local Similarity 99.2%; Pred. No. 3.6e-285;
 Matches 594; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MVOQTRPSPWIIICYYIMLGFATGGAQAQAEVLLDLSKAQOTELMISPPSGMEISG 60
 DB 1 MVOQTRPSPWIIICYYIMLGFATGGAQAQAEVLLDLSKAQOTELMISPPSGMEISG 60
 QY 61 LDENVTPIRITYQVQVMEPNQNNMLRTNWSKNAQRIPELKTLLADCNLPGVIGTCK 120
 DB 61 LDENVTPIRITYQVQVMEPNQNNMLRTNWSKNAQRIPELKTLLADCNLPGVIGTCK 120
 QY 121 ETEFLYYETDVTGKRIENLYVKIDTIAADESFTQDGERKMLNTEVREIGPLSKK 180
 DB 121 ETEFLYYETDVTGKRIENLYVKIDTIAADESFTQDGERKMLNTEVREIGPLSKK 180
 QY 181 GFYLAFQDVACIALSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVIGTCVSSABE 240
 DB 181 GFYLAFQDVACIALSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVIGTCVSSABE 240
 QY 241 EAENSPPMHCSAEGEMLVPIGKICIKAGYQOKGDTCEPGRRFPKSSSDOLQSCRPTHS 300
 DB 241 EAENSPPMHCSAEGEMLVPIGKICIKAGYQOKGDTCEPGRRFPKSSSDOLQSCRPTHS 300
 QY 301 FSDREGSSRCECEDGYRAPSDDPPYACTRPPSAPQNLFININQTVLSLESPPADNGR 360
 DB 301 FSDREGSSRCECEDGYRAPSDDPPYACTRPPSAPQNLFININQTVLSLESPPADNGR 360
 QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTVMDLLAHANFTVEEAVNG 420
 DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTVMDLLAHANFTVEEAVNG 420
 QY 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGWKEKERVLSVOLSWQEPBHPN3VITEYEIKY 480
 DB 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGWKEKERVLSVOLSWQEPBHPN3VITEYEIKY 480
 QY 481 YEKQQRERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSPPRLDVATLEBASG 540
 DB 481 YEKQQRERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSPPRLDVATLEBASG 540

QY 541 KMFETAVSSSEONPVIIIAVAVAGTIIIVFMVGFIIIGRRHCGYSKADQSGDELYFH 599
DB 540 ----ATVSSSEONPVIIIAVAVAGTIIIVFMVGFIIIGRRHCGYSKADQSGDELYFH 594

RESULT 9

US-08-449-645A-17
Sequence 17, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine
NUMBER OF INVENTIONS: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBM
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449, 645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-17

Query Match 96.8%; Score 3139; DB 2; Length 998;
Best Local Similarity 97.7%; Pred. No. 5.4e-284;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVVQTRPSPWIIICYYIWLGFHAGTGEAQAKEVLLDLSKAQOQTELEWISSPSPGMEETISG 60
DB 1 MVQTRPSPWIIICYYIWLGFHAGTGEAQAKEVLLDLSKAQOQTELEWISSPSPGMEETISG 60
QY 121 ETPFLYYETDYPDGRNIRENLVYKIDTIADESFTQDGERMKKNTREIREIGPLSKK 180
DB 121 ETPFLYYETDYPDGRNIRENLVYKIDTIADESFTQDGERMKKNTREIREIGPLSKK 180
QY 181 GFYLAFDVACIALVSVKYYKKCWITVENLAVPDDTVTGSSEFSSLVEVRGTCVSSAEE 240
DB 181 GFYLAFDVACIALVSVKYYKKCWITVENLAVPDDTVTGSSEFSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPMHGSAEGBEMLVPIGKCI CKAGYQOKGDTCEPCGRRFRKSSSODLQCSRCPHIS 300
DB 241 EAENAPRPHCSAEGBEMLVPIGKCI CKAGYQOKGDTCEPCGRRFRKSSSODLQCSRCPHIS 300
QY 301 FSDREGSSRCCEGDYRAPSDPPYVACTRPPSAPONLFININOTVSLSEMSPPADNGR 360
DB 301 FSDREGSSRCCEGDYRAPSDPPYVACTRPPSAPONLFININOTVSLSEMSPPADNGR 360
QY 361 NDVTYRILCKRCSWEGECVPCGSGNIGMPQOTGLIEDNYTVMDLLAHANTTFEVEAVNG 420
DB 361 NDVTYRILCKRCSWEGECVPCGSGNIGMPQOTGLIEDNYTVMDLLAHANTTFEVEAVNG 420

QY 421 VSDLSRQRLFAAVSIITGQAPSPQSGVMKERVLSQSVQSPPEHPNVTIEYEIKY 480
DB 421 VSDLSRQRLFAAVSIITGQAPSPQSGVMKERVLSQSVQSPPEHPNVTIEYEIKY 480
QY 481 YEKDQRERTYSTLTKSTASINNLKPGTYVFOIRAVTAAGYNSPRLVATLEASG 540
DB 481 YEKDQRERTYSTLTKSTASINNLKPGTYVFOIRAVTAAGYNSPRLVATLEASG 540
QY 541 KMFETAVSSSEONPVIIIAVAVAGTIIIVFMVGFIIIGRRHCGYSKADQSGDELYFH 599
DB 541 KMFETAVSSSEONPVIIIAVAVAGTIIIVFMVGFIIIGRRHCGYSKADQSGDELYFH 599

RESULT 10

US-08-702-367A-17
Sequence 17, Application US/08702367A
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBM
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367A-17

Query Match 96.8%; Score 3139; DB 2; Length 998;
Best Local Similarity 97.7%; Pred. No. 5.4e-284;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVVQTRPSPWIIICYYIWLGFHAGTGEAQAKEVLLDLSKAQOQTELEWISSPSPGMEETISG 60
DB 1 MVQTRPSPWIIICYYIWLGFHAGTGEAQAKEVLLDLSKAQOQTELEWISSPSPGMEETISG 60
QY 121 ETPFLYYETDYPDGRNIRENLVYKIDTIADESFTQDGERMKKNTREIREIGPLSKK 180
DB 121 ETPFLYYETDYPDGRNIRENLVYKIDTIADESFTQDGERMKKNTREIREIGPLSKK 180
QY 181 GFYLAFDVACIALVSVKYYKKCWITVENLAVPDDTVTGSSEFSSLVEVRGTCVSSAEE 240
DB 181 GFYLAFDVACIALVSVKYYKKCWITVENLAVPDDTVTGSSEFSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPMHGSAEGBEMLVPIGKCI CKAGYQOKGDTCEPCGRRFRKSSSODLQCSRCPHIS 300
DB 241 EAENAPRPHCSAEGBEMLVPIGKCI CKAGYQOKGDTCEPCGRRFRKSSSODLQCSRCPHIS 300

QY 301 FSDREGSSRCECEDGYRAPSDDPYVACTRPPSAPQNLIFINQTTVLSLEWSPPADNGR 360
 Db 301 FSDREGSSRCECEDGYRAPSDDPYVACTRPPSAPQNLIFINQTTVLSLEWSPPADNGR 360
 QY 361 NDVTYRLICRCRCSMEQGECPGCSNIGYMPQGTGLDNDYTVWDLAHANYTFEVAVNG 420
 Db 361 NDVTYRLICRCRCSMEQGECPGCSNIGYMPQGTGLDNDYTVWDLAHANYTFEVAVNG 420
 QY 421 VSDLSRQRLFAAVSITTTGQAPSOVSGWKEKERVLSQVLSMOEPHPNGVITEYEIKY 480
 Db 421 VSDLSRQRLFAAVSITTTGQAPSOVSGWKEKERVLSQVLSMOEPHPNGVITEYEIKY 480
 QY 481 YEKQRRRTYSTVTKSTSTASINNLKPGTYVVFQIRAFTAAGYGNYSPPRLVATLEBATG 540
 Db 481 YEKQRRRTYSTVTKSTSTASINNLKPGTYVVFQIRAFTAAGYGNYSPPRLVATLEBATG 540
 QY 541 KMEFATVSSSEQNPIIINAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFH 599
 Db 541 KMEFATVSSSEQNPIIINAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFH 599

RESULT 11

US-09-949-016-6501
 ; Sequence 6501, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6501
 ; LENGTH: 998
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-6501

Query Match 96.8%; Score 3139; DB 4; Length 998;

Best Local Similarity 97.7%; Pred. No. 5,4e-284;

Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVVQTRPSPWIIICYLWILGFAHTGEAOAKEVLLDLSKAQOTLEWISSPPSGMEIISG 60
 Db 1 MVVQTRPSPWIIICYLWILGFAHTGEAOAKEVLLDLSKAQOTLEWISSPPSGMEIISG 60
 QY 61 LDENYTPIRITYQVCQVMEPNQNNMLRTNWSKGAQRI FVELKFTLRDNCNSLPGVLTGCK 120
 Db 61 LDENYTPIRITYQVCQVMEPNQNNMLRTNWSKGAQRI FVELKFTLRDNCNSLPGVLTGCK 120
 QY 121 ETFTNLYYETDYGNNIRENLVYKIDTTIADESFTQGLGERKMKLNTVEIREIGPLSKK 180
 Db 121 ETFTNLYYETDYGNNIRENLVYKIDTTIADESFTQGLGERKMKLNTVEIREIGPLSKK 180
 QY 181 GFYLAPODVGACIALVSVKYYKKCWTIVENLAVFPDTVTGSRFSSLVEVRGTCVSSAEE 240
 Db 181 GFYLAPODVGACIALVSVKYYKKCWTIVENLAVFPDTVTGSRFSSLVEVRGTCVSSAEE 240
 QY 241 EAENSPPMHCSAEGEWLVPITGCKICKAGYQOKGDTCEPCGRFRFYKSSQFLQCSRCPTHS 300
 Db 241 EAENSPPMHCSAEGEWLVPITGCKICKAGYQOKGDTCEPCGRFRFYKSSQFLQCSRCPTHS 300
 QY 301 FSDREGSSRCECEDGYRAPSDDPYVACTRPPSAPQNLIFINQTTVLSLEWSPPADNGR 360
 Db 301 FSDREGSSRCECEDGYRAPSDDPYVACTRPPSAPQNLIFINQTTVLSLEWSPPADNGR 360

Db 301 FSDREGSSRCECEDGYRAPSDDPYVACTRPPSAPQNLIFINQTTVLSLEWSPPADNGR 360
 QY 361 NDVTYRLICRCRCSMEQGECPGCSNIGYMPQGTGLDNDYTVWDLAHANYTFEVAVNG 420
 Db 361 NDVTYRLICRCRCSMEQGECPGCSNIGYMPQGTGLDNDYTVWDLAHANYTFEVAVNG 420
 QY 421 VSDLSRQRLFAAVSITTTGQAPSOVSGWKEKERVLSQVLSMOEPHPNGVITEYEIKY 480
 Db 421 VSDLSRQRLFAAVSITTTGQAPSOVSGWKEKERVLSQVLSMOEPHPNGVITEYEIKY 480
 QY 481 YEKQRRRTYSTVTKSTSTASINNLKPGTYVVFQIRAFTAAGYGNYSPPRLVATLEBATG 540
 Db 481 YEKQRRRTYSTVTKSTSTASINNLKPGTYVVFQIRAFTAAGYGNYSPPRLVATLEBATG 540
 QY 541 KMEFATVSSSEQNPIIINAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFH 599
 Db 541 KMEFATVSSSEQNPIIINAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFH 599

RESULT 12

PCT-US95-04681-17
 ; Sequence 17, Application PC/TUS9504681
 ; GENERAL INFORMATION:
 ; APPLICANT: Fox, Gary M.
 ; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
 ; NUMBER OF INVENTIONS: Kinases
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Patent Operations/RBW
 ; STREET: 1840 Dehavenland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 91320
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/04681
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Winter, Robert B.
 ; REFERENCE/DOCKET NUMBER: A-287
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 998 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-04681-17

Query Match 96.8%; Score 3139; DB 5; Length 998;

Best Local Similarity 97.7%; Pred. No. 5,4e-284;

Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVVQTRPSPWIIICYLWILGFAHTGEAOAKEVLLDLSKAQOTLEWISSPPSGMEIISG 60
 Db 1 MVVQTRPSPWIIICYLWILGFAHTGEAOAKEVLLDLSKAQOTLEWISSPPSGMEIISG 60
 QY 61 LDENYTPIRITYQVCQVMEPNQNNMLRTNWSKGAQRI FVELKFTLRDNCNSLPGVLTGCK 120
 Db 61 LDENYTPIRITYQVCQVMEPNQNNMLRTNWSKGAQRI FVELKFTLRDNCNSLPGVLTGCK 120
 QY 121 ETFTNLYYETDYGNNIRENLVYKIDTTIADESFTQGLGERKMKLNTVEIREIGPLSKK 180
 Db 121 ETFTNLYYETDYGNNIRENLVYKIDTTIADESFTQGLGERKMKLNTVEIREIGPLSKK 180
 QY 181 GFYLAPODVGACIALVSVKYYKKCWTIVENLAVFPDTVTGSRFSSLVEVRGTCVSSAEE 240
 Db 181 GFYLAPODVGACIALVSVKYYKKCWTIVENLAVFPDTVTGSRFSSLVEVRGTCVSSAEE 240

QY 241 EAENAPRMHCSAEGEWLVP1GKCI CKAGYQOKGDTCEPCGRRFYKSSSODLQCRCPHIS 300
DB 241 EAENAPRMHCSAEGEWLVP1GKCI CKAGYQOKGDTCEPCGRRFYKSSSODLQCRCPHIS 300
QY 301 FSDREGSSRCCEGDGYRAPSDPYVACTRPPAPQULFININOTVLSLMSPPADNGR 360
DB 301 FSDREGSSRCCEGDGYRAPSDPYVACTRPPAPQULFININOTVLSLMSPPADNGR 360
QY 361 NDVTYRILCKRCGMEQCEVCPCGSGNIGMPQOTGLEBNYTVMDLHANATFEVEAVNG 420
DB 361 NDVTYRILCKRCGMEQCEVCPCGSGNIGMPQOTGLEBNYTVMDLHANATFEVEAVNG 420
QY 421 VSDLSRQRLFAVSIITGQAAPSOVSGVKMERVLQSRVLSMOEPHPNGVITEYEIKY 480
DB 421 VSDLSRQRLFAVSIITGQAAPSOVSGVKMERVLQSRVLSMOEPHPNGVITEYEIKY 480
QY 481 YEKQRRERTYSTVTKSTASINNLKPGTYVVFQIRAVTAAGYGNYSPLDVAATLEASG 540
DB 481 YEKQRRERTYSTVTKSTASINNLKPGTYVVFQIRAVTAAGYGNYSPLDVAATLEASG 540
QY 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599
DB 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599

RESULT 13

US-09-949-016-9901
Sequence 9901, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9901
LENGTH: 1005
TYPE: PRT
ORGANISM: Human
US-09-949-016-9901

Query Match 96.8%; Score 3139; DB 4; Length 1005;

Best Local Similarity 97.7%; Pred. No. 5.4e-284;

Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVVGTREPSMIIICYLWLGFAHTGBOAAKEVLLDSKAQOTLELWISSPPGMBEISG 60
DB 8 MVVGTREPSMIIICYLWLGFAHTGBOAAKEVLLDSKAQOTLELWISSPPGMBEISG 67
QY 61 LDENVYPIRTYOVCOVMEPNQNMRLRTNWSKGAORIFVLEKFTLRDCNSLPGLVGTCK 120
DB 68 LDENVYPIRTYOVCOVMEPNQNMRLRTNWSKGAORIFVLEKFTLRDCNSLPGLVGTCK 127
QY 121 ETFLVLYYEDYDGNIRNRELYKIDTIADESEFTQGLGERKMKLNTVEIREIGPLSK 180
DB 128 ETFLVLYYEDYDGNIRNRELYKIDTIADESEFTQGLGERKMKLNTVEIREIGPLSK 187
QY 181 GFYLAPODVAGACIALVSVKVVYKKCMWTIVENLAVFPPTVTSSESSSLVEVAGTCSAAE 240
DB 188 GFYLAPODVAGACIALVSVKVVYKKCMWTIVENLAVFPPTVTSSESSSLVEVAGTCSAAE 247
QY 241 EAENAPRMHCSAEGEWLVP1GKCI CKAGYQOKGDTCEPCGRRFYKSSSODLQCRCPHIS 300

DB 248 EAENAPRMHCSAEGEWLVP1GKCI CKAGYQOKGDTCEPCGRRFYKSSSODLQCRCPHIS 307
QY 301 FSDREGSSRCCEGDGYRAPSDPYVACTRPPAPQULFININOTVLSLMSPPADNGR 360
DB 308 FSDREGSSRCCEGDGYRAPSDPYVACTRPPAPQULFININOTVLSLMSPPADNGR 367
QY 361 NDVTYRILCKRCGMEQCEVCPCGSGNIGMPQOTGLEBNYTVMDLHANATFEVEAVNG 420
DB 368 NDVTYRILCKRCGMEQCEVCPCGSGNIGMPQOTGLEBNYTVMDLHANATFEVEAVNG 427
QY 421 VSDLSRQRLFAVSIITGQAAPSOVSGVKMERVLQSRVLSMOEPHPNGVITEYEIKY 480
DB 428 VSDLSRQRLFAVSIITGQAAPSOVSGVKMERVLQSRVLSMOEPHPNGVITEYEIKY 487
QY 481 YEKQRRERTYSTVTKSTASINNLKPGTYVVFQIRAVTAAGYGNYSPLDVAATLEASG 540
DB 488 YEKQRRERTYSTVTKSTASINNLKPGTYVVFQIRAVTAAGYGNYSPLDVAATLEASG 547
QY 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599
DB 548 KMEFATVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 606

RESULT 14

US-08-449-645A-13

Sequence 13, Application US/08449645A

Patent No. 5981245

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Denavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,645A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 991 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-449-645A-13

Query Match 56.8%; Score 1843; DB 2; Length 991;

Best Local Similarity 56.9%; Pred. No. 7.3e-163;

Matches 347; Conservative 98; Mismatches 135; Indels 30; Gaps 9;

QY 6 RFPSW--IICLYWLGFAHTGBOAAKEVLLDSKAQOTLELWISSPPGMBEISGLDE 63
DB 13 RFPSW--IICLYWLGFAHTGBOAAKEVLLDSKAQOTLELWISSPPGMBEISGLDE 67
QY 64 NYPIRTYOVCOVMEPNQNMRLRTNWSKGAORIFVLEKFTLRDCNSLPGLVGTCKET 123
DB 68 NYPIRTYOVCOVMEPNQNMRLRTNWSKGAORIFVLEKFTLRDCNSLPGLVGTCKET 127
QY 124 NLVYETDVTGNGIRNRELYKIDTIADESEFTQGLGERKMKLNTVEIREIGPLSKKGFY 183

Db 128 NMIFYESDDONGRNKIKENQYIKIDITIAADSSFTFELDLGDRVMKLNTEVRDV3PLSKKGFY 187
QY 184 LAFQDVACIALYSVKYYKKCWITIVENLAVFPDVTGSEFSSLVEVRGTC/SSAEEAE 243
Db 188 LAFQDVACIALYSVRYKKCPVVRHLAVFPDITIGADSSQLLEVSQCVN--HSVTD 245
QY 244 NSPRMHCASAGEWLVPIGKICAKAGYQOKGDTCEPCGRFRFYKSSQDLQCSRCPTHSFSD 303
Db 246 EPRMHCASAGEWLVPIGKICAKAGYEEKNGTCQVCRPFKASPHIQSCGKCPHSHYTH 305
QY 304 REGSSRCECEGYYRASPDPVYACTRPPSAPQNLININQTVLSLEWSPADNGGRNDV 363
Db 306 EEAISTCVCCEKDYFRRESDPPTMACTRPSPAPRNALSNVNETSVFLEMIPRADTGGRKDV 365
QY 364 TYRILCKRCSEWQEGECVPCGSNIGYMPQOTGLENDNYTVMDLAAHANYTEVEAVNGVSD 423
Db 366 SYIACKCKNSHAGVCECGHVRYLPQSGLNKTSVMWMDLLAHNTYFEIEAVNGVSD 425
QY 424 LSRQRLFAAVSITTTGQAAPSOVSQVKKERYLQRSVQLSWQEPHNGVITEYIKYEEK 483
Db 426 LSPGARQYVSVNVTNQAAAPSPVNNVKKGIANKSISLSWQEPDRPGIILLEYEIKHFEK 485
QY 484 DORERTYSLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNVSPRLDVAITLEASGKMF 543
Db 486 DQ-ETSTYTIKSKETTTTAEGLKPAASYVFOIRAKTAAGVFSRRFE-----F 533
QY 544 EAT---AVSSEQNPVITIIAVVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDEE-LYFH 599
Db 534 ETPVFAASDQSQIPVIAVSVTG-VILLAVIGVLLSGRCGYSAKQDPEEKKMHFH 592
QY 600 SLVTNEHLAV 609
Db 593 ----NGHIKL 598

RESULT 15
US-08-702-367A-13
; Sequence 13, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 991 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-367A-13

Query Match 56.8%; Score 1843; DB 2; Length 991;
Best Local Similarity 56.9%; Pred. No. 7,3e-163;

Matches 347; Conservative 98; Mismatches 135; Indels 30; Gaps 9;
QY 6 RFPSSW--IILCYIWLGFHTGAEQAQAEVLLDLSKAQOTLEWISSPSPGWEISGLDE 63
Db 13 RAFLMTCLLC-----AARTLLAPSNVEYNLLDSTVMGDLGWIAPPKMGWEIGEVDE 67
QY 64 NYPIRTYQVCQMEPNQNNMLFTNWSKNAORIVELKFTLRDQNSLPVUGTCKETP 123
Db 68 NYAPIHTYQVCQMEQNNMLTSMWISNEGASRIEIEKFTLRDQNSLPGGIGTCKETP 127
QY 124 NLVYFEDVDYQGNIRENLYVKIIDIITIAADESFTQGLGGERKMLNTEVEIRIGPLSKKGFY 183
Db 128 NMIFYESDDONGRNKIKENQYIKIDITIAADSSFTFELDLGDRVMKLNTEVRDV3PLSKKGFY 187
QY 184 LAFQDVACIALYSVKYYKKCWITIVENLAVFPDVTGSEFSSLVEVRGTCVSSAEEAE 243
Db 188 LAFQDVACIALYSVRYKKCPVVRHLAVFPDITIGADSSQLLEVSQCVN--HSVTD 245
QY 244 NSPRMHCASAGEWLVPIGKICAKAGYQOKGDTCEPCGRFRFYKSSQDLQCSRCPTHSFSD 303
Db 246 EPRMHCASAGEWLVPIGKICAKAGYEEKNGTCQVCRPFKASPHIQSCGKCPHSHYTH 305
QY 304 REGSSRCECEGYYRASPDPVYACTRPPSAPQNLININQTVLSLEWSPADNGGRNDV 363
Db 306 EEAISTCVCCEKDYFRRESDPPTMACTRPSPAPRNALSNVNETSVFLEMIPRADTGGRKDV 365
QY 364 TYRILCKRCSEWQEGECVPCGSNIGYMPQOTGLENDNYTVMDLAAHANYTEVEAVNGVSD 423
Db 366 SYIACKCKNSHAGVCECGHVRYLPQSGLNKTSVMWMDLLAHNTYFEIEAVNGVSD 425
QY 424 LSRQRLFAAVSITTTGQAAPSOVSQVKKERYLQRSVQLSWQEPHNGVITEYIKYEEK 483
Db 426 LSPGARQYVSVNVTNQAAAPSPVNNVKKGIANKSISLSWQEPDRPGIILLEYEIKHFEK 485
QY 484 DORERTYSLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNVSPRLDVAITLEASGKMF 543
Db 486 DQ-ETSTYTIKSKETTTTAEGLKPAASYVFOIRAKTAAGVFSRRFE-----F 533
QY 544 EAT---AVSSEQNPVITIIAVVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDEE-LYFH 599
Db 534 ETPVFAASDQSQIPVIAVSVTG-VILLAVIGVLLSGRCGYSAKQDPEEKKMHFH 592
QY 600 SLVTNEHLAV 609
Db 593 ----NGHIKL 598

Search completed: August 23, 2005, 08:27:34
Job time : 23.2217 secs

XX Example 1; Page 109-111; 128pp; English.
 PS
 CC CDNA cloning using adult mouse brains and Northern blotting identified 2
 CC truncated versions, MDK1 T1 (AAW03422) and MDK1 T2 (AAW03423), of the
 CC novel mouse developmental kinase 1 (MDK1) (see also AAW03421), a new
 CC member of the eck/eph family of receptor tyrosine kinases. Their amino
 CC acid sequences were deduced from cDNA clones (AA132961 and AA132962)
 CC obtd. from adult mouse brains. MDK T1 and T2 each possesses the entire
 CC ectodomain, the transmembrane domain and part of the juxtamembrane region
 CC of MDK1, but lack the catalytic tyrosine kinase domain. They can be used
 CC to screen for potential agents useful for treatment of diseases
 CC characterised by abnormal signal transduction
 CC
 XX

Sequence 610 AA;

Query Match 100.0%; Score 3243; DB 2; Length 610;
 Best Local Similarity 100.0%; Pred. No. 2.3e-275;
 Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVVQTRPPSWIIICYLWLGFAHTGEAQAKEVLLDLSKAQOTELEWISSPPSGMERISG 60
 DB 1 MVVQTRPPSWIIICYLWLGFAHTGEAQAKEVLLDLSKAQOTELEWISSPPSGMERISG 60
 QY 61 LDENVTPIRTYQVCQWEPNQNMLRTNWSKNAORIFVELKFTLRDCKSLPGVLTGCK 120
 DB 61 LDENVTPIRTYQVCQWEPNQNMLRTNWSKNAORIFVELKFTLRDCKSLPGVLTGCK 120
 QY 121 ETEFNLYYETDYDTGRNIRENLVYKIDTIAADESFTQGDIGERRMKLNTVREIGPLSKK 180
 DB 121 ETEFNLYYETDYDTGRNIRENLVYKIDTIAADESFTQGDIGERRMKLNTVREIGPLSKK 180
 QY 181 GFYLAFQDVACIALVSVKYYKKCWITIVENLAVFPDVTVGSEFSSSLVEVRGTCVSSAE 240
 DB 181 GFYLAFQDVACIALVSVKYYKKCWITIVENLAVFPDVTVGSEFSSSLVEVRGTCVSSAE 240
 QY 241 EAENSPPMHCSABGEWLVPIGKCTCKAGYQOKGDTCEPCGRRPYKSSSOLQSCRCTHS 300
 DB 241 EAENSPPMHCSABGEWLVPIGKCTCKAGYQOKGDTCEPCGRRPYKSSSOLQSCRCTHS 300
 QY 301 FSDREGSSRCECEGGYRAPSDPPYVACTPPSAPOULFININQTTVSLFMSPPADNGGR 360
 DB 301 FSDREGSSRCECEGGYRAPSDPPYVACTPPSAPOULFININQTTVSLFMSPPADNGGR 360
 QY 361 NDVTYRILCKRCSWEQCEVCPCGSNIGYMPQOTGLIEDNYVTVMDLAAHAYTTEVEAVNG 420
 DB 361 NDVTYRILCKRCSWEQCEVCPCGSNIGYMPQOTGLIEDNYVTVMDLAAHAYTTEVEAVNG 420
 QY 421 VSDLSRQRLFAVSTTTGQAAPSOVSQWKEKERVQSRVQLSWQEPHPGVITTEYIKY 480
 DB 421 VSDLSRQRLFAVSTTTGQAAPSOVSQWKEKERVQSRVQLSWQEPHPGVITTEYIKY 480
 QY 481 YEKDQRRRTYSTLTKSTASINNLKPGTYVFOIRVATAGYGNVSPRIDVATLEASG 540
 DB 481 YEKDQRRRTYSTLTKSTASINNLKPGTYVFOIRVATAGYGNVSPRIDVATLEASG 540
 QY 541 KMEEATVSSSEONVIIIAVAVAGTIIIVFWVGFIIIGRRHCGYSKADDEGDELYFHS 600
 DB 541 KMEEATVSSSEONVIIIAVAVAGTIIIVFWVGFIIIGRRHCGYSKADDEGDELYFHS 600
 QY 601 LVTNEHLSTL 610
 DB 601 LVTNEHLSTL 610

RESULT 2
 ID AAW03423 standard; protein; 626 AA.
 XX
 AC AAW03423;
 XX
 XX 11-NOV-1996 (first entry)

DE Mouse developmental kinase 1 MDK1 T2.

KM Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase; RTK;
 KW signal transduction; probe; diagnosis; gene therapy; neurodegeneration;
 KM neuroproliferation, cancer.

XX Mus sp.

OS

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DB 181 GFYLAPODVAGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAEE 240
QY 241 EAENSPPMHCSABGEMLVPIGKCI CKAGYQOKGPTCEPCGRFRFKSSSODLQCSRCPH 300
DB 241 EAENSPPMHCSABGEMLVPIGKCI CKAGYQOKGPTCEPCGRFRFKSSSODLQCSRCPH 300
QY 301 FSDREGSSRCCECDGYRAPSDPPYVACTRPPAPQNLIFINOTTVLSLEMSPPADNGGR 360
DB 301 FSDREGSSRCCECDGYRAPSDPPYVACTRPPAPQNLIFINOTTVLSLEMSPPADNGGR 360
QY 361 NDVTYRILCKRCSEWGECEVPCGSGNIGYMPQOTGLEBNYTVMDLLAHANTTFEVAVNG 420
DB 361 NDVTYRILCKRCSEWGECEVPCGSGNIGYMPQOTGLEBNYTVMDLLAHANTTFEVAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGAAPSOVGVKMERVLQSRVLSWQEPHPNGVITEYEIKY 480
DB 421 VSDLSRSQRLFAAVSITTTGAAPSOVGVKMERVLQSRVLSWQEPHPNGVITEYEIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVVYVFOIRAVTAAGYGNYSRPLDVALTEEASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVVYVFOIRAVTAAGYGNYSRPLDVALTEEASG 540
QY 541 KMFPAIVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDELYFHS 600
DB 541 KMFPAIVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDELYFHS 600
QY 601 L 601
DB 601 L 601

RESULT 3

ID AAM03421 standard; protein: 998 AA.
AC AAM03421;
XX 11-NOV-1996 (first entry)
DT XX
XX Mouse developmental kinase 1.
DE Mouse developmental kinase 1.
XX Mouse developmental kinase 1; MDK1; receptor tyrosine kinase; RTK;
KM signal transduction; probe; diagnosis; therapy; neurodegeneration;
KM neuroproliferation; cancer.
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT Modified-site /label= sig_peptide
FT Modified-site /label= N-glycosylation_site
FT Modified-site /label= N-glycosylation_site
FT Modified-site /label= N-glycosylation_site
FT Domain 555..579
FT /label= transmembrane_domain
XX
XX WO9621013-A1.
XX
XX 11-JUL-1996.
XX
XX 03-JAN-1996. 96WO-US000419.
XX
XX 03-JAN-1995; 95US-00368776.
XX
XX (SUGC-) SUGEN INC.
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX Clobesek T, Ullrich A, Millaer B;
XX

DR WPI: 1996-333988/33.
DR N-PSDB; AAT32960.
XX
PT New mouse development kinase 1 gene - used for developing prods. for
PT diagnosis and treatment of abnormalities in signal transduction pathways.
XX
PS Example 1; Page 105-108; 128pp; English.
XX
CC Mouse developmental kinase 1 (MDK1) (AAM03421) is a new member of the
CC eck/eph family of receptor tyrosine kinases (RTKs). Its amino acid
CC sequence was deduced from a cDNA clone (AAT32960) isolated from mouse
CC embryo and adult brain libraries. The distinct patterns of MDK1
CC expression during mouse development suggest an important role for MDK1 in
CC the formation of neuronal structures. MDK1 may be obtd. by expression in
CC host cells. It can be used in methods for the diagnosis of diseases
CC characterised by abnormality in a signal transduction pathway, such as
CC neuroproliferative or neurodegenerative disorders or cancer, to screen
CC for (ant)agonists, and to raise antibodies
XX
SQ Sequence 998 AA;

Query Match 98.4%; Score 3191; DB 2; Length 998;
Best Local Similarity 100.0%; Pred. No. 1,8e-270; Indels 0; Gaps 0;
Matches 599; Conservative 0; Mismatches 0;

QY 1 MVVQTRPSPWIIICYLWLGFAHTGEAQAKEYLLDLSKAQTELEWISSPPSGMEIRSG 60
DB 1 MVVQTRPSPWIIICYLWLGFAHTGEAQAKEYLLDLSKAQTELEWISSPPSGMEIRSG 60
QY 61 LDENVYPIRTYQVCQVMEPNQNNMLRTNWSKGNACRIEYELKFTLLDNCNLPGLCTCK 120
DB 61 LDENVYPIRTYQVCQVMEPNQNNMLRTNWSKGNACRIEYELKFTLLDNCNLPGLCTCK 120
QY 121 ETEFLYYEEDYDQGRNIRENLVYKIDTIADESFTQDGERMKNTREIRIGPLSKK 180
DB 121 ETEFLYYEEDYDQGRNIRENLVYKIDTIADESFTQDGERMKNTREIRIGPLSKK 180
QY 181 GFYLAPODVAGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAEE 240
DB 181 GFYLAPODVAGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAEE 240
QY 241 EAENSPPMHCSABGEMLVPIGKCI CKAGYQOKGPTCEPCGRFRFKSSSODLQCSRCPH 300
DB 241 EAENSPPMHCSABGEMLVPIGKCI CKAGYQOKGPTCEPCGRFRFKSSSODLQCSRCPH 300
QY 301 FSDREGSSRCCECDGYRAPSDPPYVACTRPPAPQNLIFINOTTVLSLEMSPPADNGGR 360
DB 301 FSDREGSSRCCECDGYRAPSDPPYVACTRPPAPQNLIFINOTTVLSLEMSPPADNGGR 360
QY 361 NDVTYRILCKRCSEWGECEVPCGSGNIGYMPQOTGLEBNYTVMDLLAHANTTFEVAVNG 420
DB 361 NDVTYRILCKRCSEWGECEVPCGSGNIGYMPQOTGLEBNYTVMDLLAHANTTFEVAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGAAPSOVGVKMERVLQSRVLSWQEPHPNGVITEYEIKY 480
DB 421 VSDLSRSQRLFAAVSITTTGAAPSOVGVKMERVLQSRVLSWQEPHPNGVITEYEIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVVYVFOIRAVTAAGYGNYSRPLDVALTEEASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVVYVFOIRAVTAAGYGNYSRPLDVALTEEASG 540
QY 541 KMFPAIVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDELYFHS 599
DB 541 KMFPAIVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDELYFHS 599

RESULT 4

ID ADM87167 standard; protein: 945 AA.
AC ADM87167;
XX
XX 03-JUN-2004 (first entry)
DT

XX Human protein SEQ ID NO:260.
DE
XX
XX respiratory; cytoskeletal; antiarthritic; antiinflammatory;
KM gastrointestinal; antibacterial; immunosuppressive; antididiabetic;
KM antineuritic; gene therapy; molecular weight marker; chromosome marker;
KM chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KM inflammatory condition; arthritis; inflammatory bowel disease;
KM Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KM graft versus host disease; human.
XX
XX Homo sapiens.
OS
XX WO2004009834-A2.
PN
XX 29-JAN-2004.
PD
XX 19-JUL-2002; 2002MO-US022858.
PF
XX 21-JUL-2001; 2001US-0306971P.
PR 28-MAR-2002; 2002US-00112944.
XX
XX (NUVE-) NUVELO INC.
PA
XX Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX WPI; 2004-143291/14.
DR N-PSDB; ADM66923.
XX
XX New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT versus host disease.
XX
XX Claim 20, SEQ ID NO 260; 591pp; English.
PS
XX The present invention describes an isolated polynucleotide (I): (a)
CC comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
CC which encodes a polypeptide with biological activity, where the
CC polynucleotide hybridises to (I) under stringent hybridisation conditions
CC or has greater than 98% sequence identity with (I). (I) has respiratory,
CC cytoskeletal, antiarthritic, antiinflammatory, gastrointestinal,
CC antibacterial, immunosuppressive, antididiabetic and antineuritic
CC activities, and can be used in gene therapy. (I) can be used for
CC generating polynucleotides encoding chimeric or fusion proteins and
CC heterologous protein sequences. The polynucleotides can be used to
CC express recombinant protein for analysis, characterisation or therapeutic
CC use; as markers for tissues in which the corresponding protein is
CC preferentially expressed; as molecular weight markers on gels; as
CC chromosome markers or tags to identify chromosomes or to map related gene
CC positions; to compare with endogenous DNA sequences in patients to
CC identify potential genetic disorders; as probes to hybridize and discover
CC genes, related DNA sequences; as a source of information to derive PCR
CC primers for genetic fingerprinting; as a probe to subtract-out known
CC sequences in the process of discovering other novel polynucleotides; for
CC selecting and making oligomers for attachment to a gene chip or other
CC support, including for examination of expression patterns; to raise anti-
CC protein antibodies using DNA immunisation techniques; and as an antigen
CC to raise anti-DNA antibodies or elicit another immune response. The
CC polynucleotides and polypeptides can also be used as nutritional sources
CC or supplements, e.g. as a protein or amino acid supplement, as a carbon
CC source, as a nitrogen source or as a source of carbohydrates. The
CC polynucleotides and polypeptides can also be used treat cancer. The
CC compositions are useful for promoting better or faster closure of non-
CC healing wounds, for the generation and regeneration of tissues, for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, and conditions resulting from
CC systemic cytokine damage. The compositions can also be used to treat
CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
CC or graft versus host disease. The present sequence represents a novel
CC human polypeptide sequence from the present invention. N.B. The sequences

CC for this patent were obtained from the USPTO web site from an equivalent
CC US patent US20040048249A1.
XX
XX
SQ Sequence 945 AA;
Query Match 96.8%; Score 3139; DB 8; Length 945;
Best Local Similarity 97.7%; Pred. No. 6, 2e-266;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
QY 1 MVTQTFPPSWIIICYYIWLGFATHTGEAQAKEYLLDLSAQOQTELEWISSPPSGWEEISG 60
DB 1 MVTQTFPPSWIIICYYIWLGFATHTGEAQAKEYLLDLSAQOQTELEWISSPPSGWEEISG 60
QY 1DENYTPIRTYQVCQVMEPEPQNMMLERTNWSKNAQRIFEVLEKFTLRDCNSLGVIGTCK 120
DB 61 1DENYTPIRTYQVCQVMEPEPQNMMLERTNWSKNAQRIFEVLEKFTLRDCNSLGVIGTCK 120
QY 121 EFTNLYYYEFTDPTGTGNIRENLYVKIDTIAADESFTQGDGGRKMLNTEVREIGPLSKK 180
DB 121 EFTNLYYYEFTDPTGTGNIRENLYVKIDTIAADESFTQGDGGRKMLNTEVREIGPLSKK 180
QY 181 GFLTAFQDVACIALYSVKYKCKWTIVENLAVPDTVTGSEFSSLVEVRGTCVSAER 240
DB 181 GFLTAFQDVACIALYSVKYKCKWTIVENLAVPDTVTGSEFSSLVEVRGTCVSAER 240
QY 241 EAEISPRMHCASAGEWLVPIGKCIKAGYQOKGDTCEPCGRPFYKSSODLQCSRCPTHS 300
DB 241 EAEISPRMHCASAGEWLVPIGKCIKAGYQOKGDTCEPCGRPFYKSSODLQCSRCPTHS 300
QY 301 FSDRESSSCCEGCDGYRAPSDPPYACIRPPAPQNLFINNOTTVSLSESPADNGR 360
DB 301 FSDRESSSCCEGCDGYRAPSDPPYACIRPPAPQNLFINNOTTVSLSESPADNGR 360
QY 361 NDVTYRILCKRCSEWEGCEVPCGSNIGWMPQGTGLBDNVTYVWDLAHANYTPEVAUNG 420
DB 361 NDVTYRILCKRCSEWEGCEVPCGSNIGWMPQGTGLBDNVTYVWDLAHANYTPEVAUNG 420
QY 421 VSDLSRSQRLFAAVSITTGQAPSOVGVNKEKRVOLRSQOEPBHPNGVITEYIKY 480
DB 421 VSDLSRSQRLFAAVSITTGQAPSOVGVNKEKRVOLRSQOEPBHPNGVITEYIKY 480
QY 481 YEKQGERRTYTKTSTASTASINNLKRGTYVYQIRAVYAAAGVNSPRLDVAITLEASG 540
DB 481 YEKQGERRTYTKTSTASTASINNLKRGTYVYQIRAVYAAAGVNSPRLDVAITLEASG 540
QY 541 KMFEATAVSSEQNPIIIVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFH 599
DB 541 KMFEATAVSSEQNPIIIVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFH 599
RESULT 5
AAR85092
ID AAR85092 standard; protein; 998 AA.
XX
AC AAR85092;
XX
XX 16-APR-1996 (first entry)
DT
XX
DE EPH-like receptor protein tyrosine kinase HEK11.
XX
KW EPH-like receptor protein tyrosine kinase; PK; HEK11;
KW human eph-like kinase; therapy; diagnosis; antibody; vector.
XX
OS Homo sapiens.
XX
PN WO9528484-A1.
XX
XX 26-OCT-1995.
PD
XX
XX 14-APR-1995; 95MO-US004681.
PF
XX
XX 15-APR-1994; 94US-00229509.
PR
XX

PA (AMGE-) AMGEN INC.
 XX Fox GM, Welcher AA, Jing S;
 XX WPI: 1995-373799/48.
 XX DR N-PSDB; AAT02947.
 XX
 PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and
 PT related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation or
 PT prodn.
 PS
 PS Claim 18; Page 71-75; 133pp; English.
 XX
 XX 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain
 CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11
 CC shows no homology to any known EPH-like receptor. Recombinant HEK
 CC receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host cells,
 CC and are used to produce antibodies (utilised in diagnostic assays), or to
 CC identify and purify ligands for HEK receptors, or therapeutically to
 CC modulate the activation of cell-associated receptors
 CC
 XX Sequence 998 AA;
 XX
 Query Match 96.8%; Score 3139; DB 2; Length 998;
 Best Local Similarity 97.7%; Pred. No. 6.8e-266;
 Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MVVOTRPPSWIIICYIMLGFARTGEAQAKEYLLDSKAQTELEWISSPPSGWEISIG 60
 DB 1 MVTOTRPPSWIIICYIMLGFARTGEAQAKEYLLDSKAQTELEWISSPPSGWEISIG 60
 QY 61 LDENVYTRIRYQVCQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDQNSLPVGLGTCK 120
 DB 61 LDENVYTRIRYQVCQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDQNSLPVGLGTCK 120
 QY 121 ETPFLYYEYDDYDGRNIRENLVYKIDTIADESFTQDGLGERKCKLNTREIREIGPLSKK 180
 DB 121 ETPFLYYEYDDYDGRNIRENLVYKIDTIADESFTQDGLGERKCKLNTREIREIGPLSKK 180
 QY 181 GFYLAPODVGACIALVSKYKYYKKCMTIVENLAEPDVTGSSSESLVEVAGTGVSSAEE 240
 DB 181 GFYLAPODVGACIALVSKYKYYKKCMTIVENLAEPDVTGSSSESLVEVAGTGVSSAEE 240
 QY 241 EAENSPPMHCSAEGEMWLVPIGKCI CKAGYQOKGDTCEPCGRFPYKSSSODLQCSRCPHS 300
 DB 241 EAENAPRMHCSAEGEMWLVPIGKCI CKAGYQOKGDTCEPCGRFPYKSSSODLQCSRCPHS 300
 QY 301 FSDREGSSRCCEGCTYRAPSDPPYVACTRPPSAPQNLIFINOTVYSLSEMSPPADNGCR 360
 DB 301 FSDREGSSRCCEGCTYRAPSDPPYVACTRPPSAPQNLIFINOTVYSLSEMSPPADNGCR 360
 QY 361 NDVYTRILCKRCSEGECEVCGSNIGMPOQTGEDYVVMVLLAHANTFEVAVNG 420
 DB 361 NDVYTRILCKRCSEGECEVCGSNIGMPOQTGEDYVVMVLLAHANTFEVAVNG 420
 QY 421 VSDLSRSQRLFAAVSITTTGAAPSOVGVKMERVLQSVOLSMQEPHEHNGVITEYEIKY 480
 DB 421 VSDLSRSQRLFAAVSITTTGAAPSOVGVKMERVLQSVOLSMQEPHEHNGVITEYEIKY 480
 QY 481 YEKQQRERTYSTLTKTSTASINNLKPGTVVFOIRAVTAAGYNNYSPRLDVATLEASG 540
 DB 481 YEKQQRERTYSTLTKTSTASINNLKPGTVVFOIRAVTAAGYNNYSPRLDVATLEASG 540
 QY 541 KMFEPATVSSSEQNVIITIAVAVAGTITLVFVFGFIIGRRHGYSSADOGDEELVFN 599
 DB 541 KMFEPATVSSSEQNVIITIAVAVAGTITLVFVFGFIIGRRHGYSSADOGDEELVFN 599

RESULT 6
 AAR85090
 ID AAR85090 standard; protein; 991 AA.
 XX
 XX AAR85090;
 XX
 DT 16-APR-1996 (first entry)
 XX
 DE EPH-like receptor protein tyrosine kinase HEK7.
 XX
 KM EPH-like receptor protein tyrosine kinase; PTK; HEK7;
 KM human eph-like kinase; therapy; diagnosis; vector; antibody.
 XX
 OS Homo sapiens.
 XX
 PN W09528484-A1.
 XX
 PD 26-OCT-1995.
 XX
 PF 14-APR-1995; 95WO-US004681.
 XX
 PR 15-APR-1994; 94US-00229509.
 XX
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Welcher AA, Jing S;
 PI WPI: 1995-373799/48.
 DR N-PSDB; AAT02947.
 XX
 PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and
 PT related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation or
 PT prodn.
 PS
 PS Claim 18; Page 54-57; 133pp; English.
 XX
 XX 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain
 CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11
 CC shows no homology to any known EPH-like receptor. Recombinant HEK
 CC receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host cells,
 CC and are used to produce antibodies (utilised in diagnostic assays), or to
 CC identify and purify ligands for HEK receptors, or therapeutically to
 CC modulate the activation of cell-associated receptors. Soluble HEK7
 CC receptor may primarily affect proliferation and/or differentiation of
 CC brain cells. pancreatic cells
 CC
 XX Sequence 991 AA;
 XX
 Query Match 56.8%; Score 1843; DB 2; Length 991;
 Best Local Similarity 56.9%; Pred. No. 4.3e-152;
 Matches 347; Conservative 98; Mismatches 135; Indels 30; Gaps 9;
 QY 6 RFPWM--IICYIMLGFARTGEAQAKEYLLDSKAQTELEWISSPPSGWEISIGDE 63
 DB 13 RAPLMTCLLIC-----AALRTLLASPSNEVNLDSRTVMDDLGIAFPKGMGEIIGVEDE 67
 QY 64 NYTPTRITYQVCQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDQNSLPVGLGTCKETF 123
 DB 64 NYAPTRITYQVCQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDQNSLPVGLGTCKETF 127
 QY 124 NLVYETDVTYDGRNIRENLVYKIDTIADESFTQDGLGERKCKLNTREIREIGPLSKKGFY 183
 DB 128 NMYEFESDDQNGRNIRENKYKIDTIADESFTQDGLGERKCKLNTREIREIGPLSKKGFY 187
 QY 184 LAPQDVACIALVSKYKYYKKCMTIVENLAEPDVTGSSSESLVEVAGTGVSSAEEAE 243
 DB 188 LAPQDVACIALVSKYKYYKKCMTIVENLAEPDVTGSSSESLVEVAGTGVSSAEEAE 245

KM neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
 KM binding protein; BDNF; NT-3; diagnosis.
 OS Rattus sp.
 PN US843749-A.
 XX
 XX
 PD 01-DEC-1998.
 XX
 PF 06-JUN-1995; 95US-00469537.
 XX
 PR 26-JUL-1991; 91US-00736559.
 PR 28-OCT-1993; 93US-0014992.
 PR 17-MAR-1995; 95US-00406247.
 XX
 PA (REG-) REGENERON PHARM INC.
 XX
 PI Maslakowski P, Yancopoulos GD, Maisompierre PC;
 XX
 XX WPI; 1999-044584/04.
 DR N-PSDB; AAV70207.
 XX
 PT DNA encoding receptor tyrosine kinase proteins - and corresponding
 PT proteins.
 XX
 PS Example; Fig 22; 194pp; English.
 XX
 XX The present invention describes nucleic acid molecules for *ror-1*, *ror-2*,
 CC *ehk-1* and *ehk-2*. Also described are the corresponding proteins: *Ror-1*,
 CC *Ror-2*, *Ehk-1*, and *Ehk-2*. The proteins are orphan receptor tyrosine
 CC kinases. The present sequence represents rat *Ehk-1*
 XX
 XX Sequence 1005 AA;
 SQ
 Query Match 56.2%; Score 1824; DB 2; Length 1005;
 Best Local Similarity 54.8%; Pred. No. 2.3e-150;
 Matches 351; Conservative 96; Mismatches 138; Indels 56; Gaps 11;
 QY 6 RFPSEWILCY-----IM-----LLGFATGDAQAAKEVLLDSKAQOQTELEWISSPPSG 54
 DB 25 RVPASLGLGCTISAPLKGPMWTLCLCALRTLLASPSNEVNLDSRTVLGDMIAFPKNG 84
 QY 55 WEBSIGDENYTPRTYQVQVMEPNQNNMLRTWISKNAQRIFEVLEKTLRDONSIPG 114
 DB 85 WEBSIGEDENVAPRIHTYQVCKVMEQNNMLTSMISMEGSRFIELEKTLRDONSIPG 144
 QY 115 VLGTCKETFNLYETDVTGSRNIRENLYKIDITIADESGTQDGLGERKKMLTEVREI 174
 DB 145 GLGTCKETFNMYEPESDDENGRNKENQYIKIDITIADESGTQDGLGERKKMLTEVADV 204
 QY 175 GPLSKGFPYLAFOVVGACIALVSVKVKKWTIVENLAVPDPVTGSEPSLVEVGTG 234
 DB 205 GPLSKGFPYLAFOVVGACIALVSVKVKKCPVVRHLAVPDPVTGADSSQLLEVGSGC 264
 QY 235 VSSAEEBAENSPRMHCAGEMLVPIGKICAKAGYQOQKGTCEPCGRFRFYKSSQDQCS 294
 DB 265 VN--HSTVDPDKPKHCAEGEMLVPIGKCMKAKAYEEENGTCYQCRGCFEFASSHQTC 322
 QY 295 RCPHSGSDREGSSRCECEDGYAPSDPPYVACTRPPSPQNLIFINOTTVLEWSP 354
 DB 323 KCPHSGYTHREASTSCVCEKDYFRRESPPPTMACTRPPSPARNAISVNETSVLEWIP 382
 QY 355 ADNGGRNDVTYRLICKKSGMEQECVPCGSNIGVMPQOTGLEDYVYVMDLAHANTFE 414
 DB 383 ADTGCGKDVSTYILCKKCNHAGVCEBGHVRLLPODGLKNTSVMMADPLAHNTNTPFE 442
 QY 415 VEAANGVSDLSRSQRLPAFVAVSITGQAAPSQVSGVMKERVLRQSVLSMOPEHPNGVIT 474
 DB 443 IEAANGVSDLSRPGROYVAVVTTNQAAPSVTVTKGKIKAKNISLSWQSPDRPNGLIL 502
 QY 475 EYEIKYIEKQDRETYTLTKTSASINNLKPGTVYVFOIRAVTAAGYNGYSPRLDVAT 534
 DB 503 EYEIKYIEKQD-ETSYIILIKSKETTLTAEGLKPAASVYVFOIRARTAGYGVSRFRFE-- 558

QY 535 LEEASGMPEFATAV---SSQNPIILAVAVAGTILVEMVRFII-----GRR- 581
 DB 559 -----FETTPVFGASNNQSQPIIGVSVTVGVILLAWMI-GFLSSGCECGCGRAS 609
 QY 582 -----HCGSKADQEGDEE-LYFHSVLVTEHLSV 609
 DB 610 SLCAVAHPSLIWRGYSKAKODPEEEKMHPH-----NGHIXL 646
 RESULT 9
 ABR44241
 ID ABR44241 standard; protein; 1037 AA.
 AC ABR44241;
 XX
 XX 18-AUG-2003 (first entry)
 DT
 DE Tyrosine kinase EHK-1.
 XX
 XX CD81; neuron; neural degeneration; astrocyte; Nr51; cytosolic; EHK-1;
 KM neuroprotective; nootropic; antiparkinsonian; anticonvulsant; human;
 KM cerebroprotective; gene therapy; tyrosine kinase.
 XX
 XX Homo sapiens.
 OS
 PN WC003040333-A2.
 XX
 PD 15-MAY-2003.
 PF 07-NOV-2002; 2002WO-US035588.
 PR 07-NOV-2001; 2001US-0344712P.
 XX
 PA (YESH) UNIV YESHIYA EINSTEIN COLLEGE.
 PI Weinstein DE, Suarez C, Zerlin M;
 XX
 DR WPI; 2003-441557/41.
 DR N-PSDB; AC078163.
 XX
 PT Enhancing survival of neurons, useful for treating neural degeneration
 PT (e.g. Alzheimer's disease) or a defect in astrocyte proliferation (e.g.
 PT astrocytosis), comprises contacting the neurons with CD81 protein or its
 PT derivative.
 XX
 PS Claim 29; Fig 28; 59pp; English.
 XX
 XX The invention relates to enhancing survival of neurons and involves
 CC contacting the neurons with CD81 protein or CD81 derivative, or its
 CC stabilized variants, in an amount that enhances survival of the neurons.
 CC The method is useful for treating neural degeneration or a condition
 CC associated with a defect in astrocyte proliferation in a mammal, and
 CC involves activating Nr51 or CD81 in the mammal. The method is useful in
 CC treating neural degeneration (e.g. Alzheimer's disease, amyotrophic
 CC lateral sclerosis, Binswanger's disease, Huntington's chorea, multiple
 CC sclerosis, myasthenia gravis, Parkinson's disease, Pick's disease,
 CC cerebral palsy, congenital hydrocephalus, muscular dystrophy, stroke or
 CC vascular dementia) or a condition associated with a defect in astrocyte
 CC proliferation, such as astrocytosis or astrocytoma. The present sequence
 CC represents a the EHK-1 protein (the Nr51 protein has been previously
 CC identified as an orphan receptor tyrosine kinase termed EHK-1-GenBank
 CC Accession No. XM_046083.2.)
 CC
 XX
 SQ Sequence 1037 AA;
 Query Match 56.2%; Score 1824; DB 6; Length 1037;
 Best Local Similarity 55.2%; Pred. No. 2.5e-150;
 Matches 349; Conservative 97; Mismatches 134; Indels 52; Gaps 11;
 QY 6 RFPSEW--IILCYWLLGFATGDAQAAKEVLLDSKAQOQTELEWISSPPGWEBISGLDE 63
 DB 37 RAPLMWTLCLC-----AALRTLLASPSNEVNLDSRTVMGDLGWIAPFKNGWEBIGVDE 91

Db 558 ETTVPFAASSDQSIPIVAVSVTVG-VILLAVIGVLSSGCCGCCGRASSLCAVAHPI 616
 QY 582 ---HCGYSKADQDEDE-LYFHSLVTVNEHLSV 609
 Db 617 LHMCGYSKAKODPEEKMHF---NGHITKL 644

RESULT 11
 ADEJ31683
 ID ADEJ31683 standard; procein; 1037 AA.
 XX ADEJ31683;
 AC ADEJ31683;
 XX 29-JAN-2004 (first entry)
 XX Human 1419 protein #SEQ ID 40.
 DE
 XX Antiarteriosclerotic; cardiant; vasotrophic; antiinflammatory;
 KM thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
 KM cardiovascular; disorder; ischaemia; aortic bending;
 KM vascular heart disease; endocarditis; atrial fibrillation; heart failure;
 KM angina; cardiomyopathy; cardiac death.
 XX Homo sapiens.
 OS
 XX MO2003065984-A2.
 PN 14-AUG-2003.
 XX 29-JAN-2003; 2003WO-US002571.
 PF
 XX 01-FEB-2002; 2002US-0353224P.
 PR 15-MAR-2002; 2002US-0354529P.
 PR 19-APR-2002; 2002US-0373861P.
 PR 29-APR-2002; 2002US-0376287P.
 PR 12-JUN-2002; 2002US-0388080P.
 PR 24-JUN-2002; 2002US-0390971P.
 PR 03-JUL-2002; 2002US-0394130P.
 PR 10-JUL-2002; 2002US-0394797P.
 PR 21-AUG-2002; 2002US-0404904P.
 PR 23-AUG-2002; 2002US-0405450P.
 PR 04-SEP-2002; 2002US-0424300P.
 PR 06-NOV-2002; 2002US-0424300P.
 PR 05-DEC-2002; 2002US-0431042P.
 PR 05-DEC-2002; 2002US-0431079P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghu M,
 PI Scaglino N, Perodin J, Rodrigue-Way A,
 XX WPI, 2003-731468/69.
 DR N-PSDB; ADEJ31682.
 XX
 PT Identifying a compound capable of treating a cardiovascular disorder
 PT (e.g. atherosclerosis) comprises assaying the ability of the compound to
 PT modulate the expression or activity of e.g. 1682, 6169 or 6193
 PT polypeptide or nucleic acid.
 XX
 PS Disclosure; SEQ ID NO 40; 328bp; English.
 XX
 CC The invention relates to a method for identifying a compound capable of
 CC treating a cardiovascular disorder. The present invention identifies the
 CC differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
 CC 43126, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 13702, 7077,
 CC 33607, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484,
 CC 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
 CC 2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,
 CC 19489, 21833, 2217, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
 CC 6585 genes in cardiovascular disease states. The methods are useful in
 CC diagnosing, preventing and treating cardiovascular disorders, such as
 CC atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,

CC restenosis, arterial inflammation, vascular wall remodeling, coronary
 CC microembolism, tachycardia, bradycardia, pressure overload, aortic
 CC bending, coronary artery ligation, vascular heart disease, valvular
 CC disease, including but not limited to, valvular degeneration caused by
 CC calcification, rheumatic heart disease, endocarditis, or complications of
 CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
 CC heart failure, sinus node dysfunction, angina, heart failure,
 CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
 CC including but not limited to, pericardial effusion and pericarditis;
 CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
 CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
 CC artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
 CC cardiovascular developmental disorders. The methods may also be used for
 CC identifying compounds that modulate cardiovascular disorders. Sequences
 CC given in ADEJ31644-ADEJ31769 represent the genes and proteins that may be
 CC regulated by a compound of the invention.
 XX
 SQ Sequence 1037 AA;
 XX
 Query Match 56.1%; Score 1819; DB 7; Length 1037;
 Best Local Similarity 55.1%; Pred. No. 6,7e-150;
 Matches 348; Conservative 98; Mismatches 134; Indels 52; Gaps 11;
 QY 6 RFPWM-IIIICYIWLGFHATGEAQAKEYLLDSKAQOTELEWISSPSSGMEISGLDE 63
 Db 37 RAPLMTGCLLC-----AALRTILASPNSNEVLDSRTVMGDLGWIAPKNGMEIEIGVDE 91
 QY 64 NYTPIRTYQVQVWPNPNMMLRTNWSKGAQXIPBLKTTLDNCSLPVLTGCKTF 123
 Db 92 NYAPIHTYQVCKWEQONMMLTWSINBEGASRIPELKTTLDRDNCNLPGLTGCKTF 151
 QY 124 NLYYETDPTDGRNIRENLVYKIDITIADESFTGSDGERMKNTREPREISPLSKGFY 183
 Db 152 NMYFESDQNGRIKENQIKITIDADESFTLIDGDRMKNTREPRDVPISKGFY 211
 QY 184 LAFQDVACIALVSVKYYKKCWITVENLAVFPDVTGSEBSLVEYRGTCVSSABEBAE 243
 Db 212 LAFQDVACIALVSVRYKKCPVNHIAVFPPTITGADSSQLLEVSGCVN--HSVTD 269
 QY 244 NSPRMCSAGEWLVPIPKGKICAKAGYQKQDTCPCRRPFKSSQDLQCRCTHSSSD 303
 Db 270 EPPRMCSAGEWLVPIPKGKICAKAGYQKQDTCPCRRPFKSSQDLQCRCTHSSSD 329
 QY 304 REGSSRCECEGYRAASDPYVACTRPPAPQNLININQTTVLSMSPRADNGRNDV 363
 Db 330 EEAISTCVCEDYFRRESDEPTMCTPPAPRAAISNVMTSVFLEIIPADTGKRDV 389
 QY 364 TYRILCRGSEWQECVPCGSNIGYMPQGTLEDDNYTVMDLLAHANYTFEVAVNGVSD 423
 Db 390 SYTLACKKNSHAGVCEGCHVAYLPKQSLKNTSVMDLANTHTYTFEIVANGVSD 449
 QY 424 LRSQRLPAVAVITGQAPDSQVSGMKERYLQSRVOLSQWQEPHPNGVITYEIKYK 483
 Db 450 LSPGARQVSVNVTNQAAPSPTNVKKGKIAKNSISLSQWQEPHPNGIILEYEIKYK 509
 QY 484 DQRERTSTLTKSTSTSNINLKPQYVPOIRVTAAGVNGVSPRLDVATLEBASGMF 543
 Db 510 DQ-ETSTIILSKETITTAAGLRASVYFQIRKRTAAGVGRFRPE-----F 557
 QY 544 EAT---AVSEONFVILIAVAVAGTILVFMVGFII-----GRR----- 581
 Db 558 ETTVPFAASSDQSIPIVAVSVTVG-VILLAVIGVLSSGCCGCCGRASSLCAVAHPI 616
 QY 582 ---HCGYSKADQDEDE-LYFHSLVTVNEHLSV 609
 Db 617 LHMCGYSKAKODPEEKMHF---NGHITKL 644

RESULT 12
 ABP5827 standard; protein; 975 AA.
 ID ABP5827
 AC ABP5827;

XX 31-OCT-2002 (first entry)
 XX Human Eph-1 receptor tyrosine kinase protein SEQ ID NO:8.
 DE Human; kinase; enzyme; inflammation; cancer; psoriasis; gene therapy;
 KM arteriosclerosis; antiinflammatory; cyostatic; antipsoriatic;
 KW antiarteriosclerotic.
 XX Homo sapiens.
 OS
 PN MO200257432-A2.
 XX
 XX 25-JUL-2002.
 PD
 XX 02-JAN-2002; 2002MO-US000112.
 PF
 XX 02-JAN-2001; 2001US-00751389.
 PR
 XX (PEKE) PE CORP.
 PA
 PI Guegler K, Webster M, Di Francesco V, Beasley EM;
 XX WPI; 2002-559718/64.
 XX
 XX New peptides encoded by genes within the human genome useful for treating
 PT disorders associated with abnormal expression of kinase, e.g.
 PT inflammation, cancer, arteriosclerosis, in drug screening assays and
 PT pharmacogenomic analysis.
 PS
 XX Disclosure; Fig 2H-J; 346pp; English.
 XX
 XX The present invention describes a human kinase protein (I), located on
 CC chromosome 3. (I) has antiinflammatory, cyostatic, antipsoriatic and
 CC antiarteriosclerotic activities, and can be used in gene therapy. (I)
 CC peptides can be used in substantial and specific assays related to
 CC functional information of the peptide sequences, to raise antibodies or
 CC to elicit immune response, as reagents in assays to determine the levels
 CC of protein in biological fluids, and as markers for tissues where the
 CC corresponding protein is expressed. The peptides and antibodies are
 CC useful in drug screening assays, tissue typing and pharmacogenomic
 CC analysis. They are also useful in treating disorders associated with the
 CC absence of, inappropriate, or unwanted expression of the kinase protein,
 CC e.g. inflammation, cancer, arteriosclerosis, and psoriasis. The nucleic
 CC acid molecules encoding (I) can be used for probes, primers and chemical
 CC intermediates in biological assays, for constructing recombinant vectors,
 CC expressing antigenic portions of the protein. The peptide and nucleic
 CC acid sequences are useful as models for the development of human
 CC therapeutic targets, aid in the identification of therapeutic proteins
 CC and serve as targets for the development of human therapeutic agents that
 CC modulate kinase activity in cells and tissues that express the kinase.
 CC The present sequence represents a protein given in comparison with the
 CC human kinase protein of the present invention
 CC
 XX
 XX Sequence 975 AA,
 SQ
 Query Match 55.8%; Score 1808.5; DB 5; length 975;
 Best Local Similarity 56.3%; Pred. No. 5.1e-149;
 Matches 341; Conservative 96; Mismatches 124; Indels 45; Gaps 9;
 QY 30 AKEVLLDSAAQOQTELEWISSPSGMEISGLDENYPIITYOVCOME:NONNMLRTNW 89
 DB 1 SNEVNLDSRTWGDLLGWIAPFKKGMEIEGVDENVAPIHITYOVCKME:NONNMLRTSW 60
 QY 90 ISNGNORIVFVELKFTLRDGNLSLPGVLGCKEKNFNLVYETDVTGINKIKENLYVKIDTI 149
 DB 61 ISNEGASRIETELKFTLRDGNLSLPGGLGCKEKNFNMIFESDDONGENIKENQYIKIDTI 120
 QY 150 AADESFTQGLGERKMKLATEVEIREIGPLSKKGFYLAFOVDGACIALYSV:CVYKKCWTIV 209
 DB 121 AADESFTQLDGRVYKMLATEVRDVGPLSKKGFYLAFOVDGACIALYSV:VYVYKKCPSV 180
 QY 210 ENLAVFPDITYGSEFSSLVVEVGTGVSSAEEBAENSPRMHCSAEGEWLV:IGKICCKAGY 269

DB 181 RHIAVFPDITYTGADSSQLLEVSQSVN:-HSVTDEPPKMGCSAEGWLV:IGKCMCKAGY 238
 QY 270 QOKGDDCEPCGRFRFYSSSODLLQCSRCPTHSFSDREGSSRCECEDGYRAPSPPVACT 329
 DB 239 EEKNGTCQVCRPEFFRASFHIGSCGKCPHRSYTHEASISCVCEKDYFRSPPTMACT 238
 QY 330 RPPSAPONTLFINQNTTSLSEWSPPADNGRNDVYRIILCKRCSWQEGECVPCGSNIGYM 389
 DB 299 RPPSAPRMAISNVERISVLEWIPADTGGRKDVSYIACKCNSHAGVCEECGHVRYL 358
 QY 390 PQOTGLEDNVYTMDLAANVTFEVEANVGSGLRSQRLFAAVITTCQAAPSOVSGV 419
 DB 359 PROSGLKNTSVMMVDLAHTNFTFELEAVNGVSDLSPGAQOYVAVVTNQAAPSPVTNV 418
 QY 450 MKERVLORSVQLSMOPEHNGVITTEYIEIKYEDKDRERTYSTLKTSASINNLKPGT 509
 DB 419 KKGIKAKNSISLSMOEPDRNGIILEYELKHFKDQ-ETSYTIILKETTITMGLKRPAS 477
 QY 510 VYVFOIRAVTAAAGYGVNSPRLDVATLEASGKMEAT--AVSEONPVIIINAVAVAGT 566
 DB 478 VYVFOIRARTAAAGYGVNSRFE-----FETTPVFAASSDOSQIPVIAVSVTVG- 525
 QY 567 IILVNVFGRIL-----GGR-----HGSYKADGEGDEE-LYFHSIVT 603
 DB 526 VILLAVVIGVLLSGSCCGCGRASSLCAVAHPILIMRCGYSAKODPEEEKVHFH--- 581
 QY 604 NEHLASV 609
 DB 582 NGHIXL 587
 RESULT 13
 AAB08665
 ID AAB08665 standard; protein; 983 AA.
 XX
 XX AAB08665;
 XX
 XX 02-JAN-2001 (first entry)
 DE Amino acid sequence of a human EphA3 HLA class II-binding peptide.
 XX
 XX EphA3, HLA class II-binding peptide; human leukocyte antigen; antigen;
 KW CD4+ T lymphocyte; tumour associated gene; vaccine.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Binding-site 1..9 HLA class I binding motif
 FT /note= "HLA class I binding motif"
 FT 47..55
 FT /note= "HLA class I binding motif"
 FT 103..111
 FT /note= "HLA class I binding motif"
 FT 149..157
 FT /note= "HLA class I binding motif"
 FT 168..176
 FT /note= "HLA class I binding motif"
 FT 459..467
 FT /note= "HLA class I binding motif"
 FT 554..562
 FT /note= "HLA class I binding motif"
 FT 558..566
 FT /note= "HLA class I binding motif"
 FT 565..573
 FT /note= "HLA class I binding motif"
 FT 589..597
 FT /note= "HLA class I binding motif"
 FT 656..664
 FT /note= "HLA class I binding motif"
 FT 675..683
 FT /note= "HLA class I binding motif"
 FT 683..691

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FT      /note= "HLA class I binding motif"
FT      Binding-site
FT      727..735
FT      /note= "HLA class I binding motif"
FT      Binding-site
FT      788..796
FT      /note= "HLA class I binding motif"
FT      Binding-site
FT      895..903
FT      /note= "HLA class I binding motif"
FT      Binding-site
FT      929..937
FT      /note= "HLA class I binding motif"
XX      W0200050589-A1.
XX      PD
XX      31-AUG-2000.
XX      PF
XX      18-FEB-2000; 2000MO-US004326.
XX      PR
XX      22-FEB-1999; 99US-0121170P.
XX      PR
XX      08-OCT-1999; 99US-0158566P.
XX      PA
XX      (LUDW-) LUDWIG INST CANCER RES.
XX      PI
XX      Chiari R, Coulie P, Boon-Falleur T;
XX      WPI; 2000-572089/53.
XX      DR
XX      N-PSDB; AAA64458.
XX      PS
XX      Novel tyrosine kinase receptor, EphA3 human leukocyte antigen (HLA) class
XX      PT II binding peptide and nucleic acid encoding the receptor, useful for
XX      PT diagnosing and treating conditions characterized by expression of EphA3
XX      PT gene.
XX      PS
XX      Claim 1; Page 81-83; 107pp; English.
XX      CC
XX      The present sequence represents a EphA3 HLA (human leukocyte antigen)
XX      CC class II-binding peptide. EphA3 antigens, when presented by an antigen
XX      CC presenting cell having a HLA class II molecule, effectively induce
XX      CC activation and proliferation of CD4+ T lymphocytes. EphA3 is a tumour
XX      CC associated gene. EphA3 HLA binding peptides are used for selectively
XX      CC enriching a population of T lymphocytes. The peptides are also used for
XX      CC diagnosing a disorder characterized by EphA3 or EphA3 HLA binding peptide
XX      CC expression. The peptides are also used to treat a disorder characterized
XX      CC by EphA3 expression. The EphA3 binding peptides are useful in producing
XX      CC vaccines and antibody
XX      CC
XX      SQ
XX      Sequence 983 AA;
XX
XX      Query Match
XX      Best Local Similarity 55.5%; Score 1799; DB 3; Length 983;
XX      Matches 332; Conservative 103; Mismatches 131; Indels 16; Gaps 6;
XX
XX      Db
XX      28 QAAKEVLLDSKQOETLEWISSPSPGMEIISGLDENVTPRTYOVQVWEPNOMNMLRT 87
XX      25 QPSNEVVLDSKTIQEGELWISYPSHGEIISGVDEHYTPRTYOVQVWDSNNMLRT 84
XX      Qy
XX      88 NWISKGAORIFVELKFTLRDCLSLPGVLGCTKETFLNLYEYETDYDGRNIRELVLKID 147
XX      Db
XX      85 NWVPRNAQKTYVELKFTLRDCLSLPGVLGCTKETFLNLYEYETDYDGRNIRELVLKID 144
XX      Qy
XX      148 TIAADESFTQDGLGERKMLNTEVREIGPLSKKGFYLAFOVAGACIALVSVKYYKKCMT 207
XX      Db
XX      145 TIAADESFTQDGLGERKMLNTEVREIGPLSKKGFYLAFOVAGACIALVSVKYYKKCMT 204
XX      Qy
XX      208 IVENLAFFPTVYVGEFSSLVENVGTQVSSAEAEASPMHGCABEEMLVPIGKICKA 267
XX      Db
XX      205 TVKNLAFFPTVYVGEFSSLVENVGTQVSSAEAEASPMHGCABEEMLVPIGKICKA 261
XX      Qy
XX      268 GYOQKGDTCPCGRFYYKSSODLQCRPTSHSFDSGSSRCEDGGYRAPSPDYVA 327
XX      Db
XX      262 GYERGMCGACRGCFYKALDGNMKCAKCPHSHSTQDGSNMGCCNNYPRADDPSPMA 321
XX      Qy
XX      328 CTRPPSPAPONLIPIINOTTYSLEWSPPADNGRNDVYTRILCKRCSWEGECVPGCSNIG 387
XX      Db
XX      322 CTRPPSPSPRVNISININETSVLIDWSWPLDTGGRKDVTFNII CKKCGNNIKCEPCSPNVR 381

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Qy      388 YMPQOTGLFDNYTYMDLALHANYFEVAVNGVSDLSRQRLFAAVSITTGQAAPSOVS 447
Db      382 FLRQFGELTNTTYTYVDLHNTHTPEIDAVNGVSELSPPRQPAVSTITNOAAPSVL 441
Qy      448 GWMKERYLQSVOLSWQEPHPNGVITEYEIKYEXKQDRERTYSTLKTSASINLKP 507
Db      442 TIKDRTSRNSISLSWQEPHPNGIILDEVKTYKEQGETSTYILARGTNVTISLKP 501
Qy      508 GTTYVFOIRAVTAAGYNTSPRLDVALTEASGKMFATVASSQONVITIIAVAVAGTI 567
Db      502 DTYVFOIRARTAGVGTNRKFEFTSP-----DSFISGSSQVMAISAVALI 554
Qy      568 ILVEMVFGFIIGRRHCGSKADQGEDELYEHSIVTNEHLSV 609
Db      555 LITVVIY-VLIG-RFCGYKSKRGADKRLHF----GNGHLKL 590
XX
XX      RESULT 14
XX      ID
XX      AAB08666 standard; protein; 983 AA.
XX      AC
XX      AAB08666;
XX      DT
XX      02-JAN-2001 (first entry)
XX      DE
XX      A human EphA3 HLA class II-binding peptide.
XX      XX
XX      EphA3; HLA class II-binding peptide; human leukocyte antigen; antigen;
XX      KW CD4+ T lymphocyte; tumour associated gene; vaccine.
XX      OS
XX      Homo sapiens.
XX      PN
XX      W0200050589-A1.
XX      PD
XX      31-AUG-2000.
XX      PF
XX      18-FEB-2000; 2000MO-US004326.
XX      PR
XX      22-FEB-1999; 99US-0121170P.
XX      PR
XX      08-OCT-1999; 99US-0158566P.
XX      PA
XX      (LUDW-) LUDWIG INST CANCER RES.
XX      PI
XX      Chiari R, Coulie P, Boon-Falleur T;
XX      WPI; 2000-572089/53.
XX      DR
XX      N-PSDB; AAA64459.
XX      PT
XX      Novel tyrosine kinase receptor, EphA3 human leukocyte antigen (HLA) class
XX      PT II binding peptide and nucleic acid encoding the receptor, useful for
XX      PT diagnosing and treating conditions characterized by expression of EphA3
XX      PT gene.
XX      PS
XX      Claim 1; Page 88-90; 107pp; English.
XX      CC
XX      The present sequence represents a EphA3 HLA (human leukocyte antigen)
XX      CC class II-binding peptide. EphA3 antigens, when presented by an antigen
XX      CC presenting cell having a HLA class II molecule, effectively induce
XX      CC activation and proliferation of CD4+ T lymphocytes. EphA3 is a tumour
XX      CC associated gene. EphA3 HLA binding peptides are used for selectively
XX      CC enriching a population of T lymphocytes. The peptides are also used for
XX      CC diagnosing a disorder characterized by EphA3 or EphA3 HLA binding peptide
XX      CC expression. The peptides are also used to treat a disorder characterized
XX      CC by EphA3 expression. The EphA3 binding peptides are useful in producing
XX      CC vaccines and antibody
XX      CC
XX      SQ
XX      Sequence 983 AA;
XX
XX      Query Match
XX      Best Local Similarity 55.5%; Score 1799; DB 3; Length 983;
XX      Matches 332; Conservative 103; Mismatches 131; Indels 16; Gaps 6;

```

QY 28 QAAKEVLLDLSKAOQTELEWISSPPSGMEISGLDENYTPRTYQVCYQVMEPNQNNWLT 87
DB 25 QPSENEVNLDSKTIQDELWISYPSHGWIEISGVDEHYTPRTYQVCNWNWLT 84
QY 88 NWSKGAORIFVELKFTLRDNCNLSLPGVLGTCRFTFLYYEENDYDGRNIRENLVKID 147
DB 85 NWPRNSAQKIYELKFTLRDNCNLSLPGVLGTCRFTFLYYEENDYDGRNIRENLVKID 144
QY 148 TIAADESFTQDGERMKLNTVEIREIGPLSKKGFYLAFOVAGACIALVSXYKKYKCKMT 207
DB 145 TIAADESFTQMDGDRILKLNTEIREVGPVNNKGFYLAFOVAGACIALVSXYKKYKCKMT 204
QY 208 IYENLAVFPPTYGSESSLYEVRGTCVSSAEBAENSPPMCHSAGEMLVPIGKICCKA 267
DB 205 IYVNLAMFPDTPV-MDSQSLVEVRGSCVNNKSKE--EDPPRMVCTSTEGEMLVPIGKICCKA 261
QY 268 GYOQKGDTCPCGRFRFYKSSODLQCRPTHSFSDRGSCRCEDDGYFAPSDPPYVA 327
DB 262 GYBERGFMCAQCRPGFYKALDGNMKCAKCPHSHSTQDGSMMNCRCENNYFLADKDPSPMA 321
QY 328 CTRPPSAPOULIFNINQTTVSLWSPPADNGRNDVTYRILCKRCWEQEGCVPCGSNTG 387
DB 322 CTRPPSPRNVISININETSVIDLWSPMDLDTGKRDVTFNILCKCGMNIKQCEPCSPNVR 381
QY 388 YMQOQTGLENNYTVMDLHANATFEVEAVNGVSDLSRQRLFAVSTITGQAAPSOVS 447
DB 382 FLPRQGLTNTVTVDDLHANTYTFEIDAANGVSELSPRQFAVSTITGQAAPSPVL 441
QY 448 GWKERVLORSVOLSMQEPHNGVITEYEIKYKQDERTYSTLTCTKS*TSASINNLKP 507
DB 442 TIKKDRSRNSISLSWQEPHNGIILDYEVKYEKQDERTYSTLTARCTNVTISLKP 501
QY 508 GTVYVFOIRAVTAAGYGNYSPLDVALTEBASGMFEATAVSSQNPVITIAVAVAGTI 567
DB 502 DTIVYFOIRARTAGYGNYSPLDVALTEBASGMFEATAVSSQNPVITIAVAVAGTI 564
QY 568 ILVFMVFGIIGRRHCGYSKADQDEGBELYFHSVLTNHELSV 609
DB 555 LITVIVY-VLIG-RFCGYKSKHGADKRLHF---GNGHLK 590

RESULT 15
ABR57491
ID ABR57491 standard; protein; 983 AA.
XX ABR57491;
AC
XX
DT 16-SEP-2003 (first entry)
XX
DE Human EphA3 protein SEQ ID NO:11.
XX
KW Human; bone and joint diseases; antiarthritic; antirheumatic; osteopathic;
KW antiinflammatory; arthritis deformans; chronic rheumatoid arthritis;
KW synovial inflammation; arthritis; tennis elbow; EphA3; Eph receptor A3.
XX
OS Homo sapiens.
XX
PN WO2003022300-A1.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-JP009140.
XX
PR 10-SEP-2001; 2001JP-00273914.
PR 17-SEP-2001; 2001JP-00281472.
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XX
PA (TAKE) TAKEDA CHEM IND LTD.
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PI Hikichi Y, Inazuka M, Yoshimura K;

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DR WPI; 2003-313193/30.
XX N-PSDB; ACF03675.
PT Substances regulating the activity of proteins having increased
PT expression in bone and joint disease for treatment and prevention of
PT these diseases.
XX
PS Claim 1; Page 132-136; 154pp; Japanese.
XX
CC The present invention describes agents (A) for treating and preventing
CC bone and joint diseases. (A) regulate the activity or expression of human
CC proteins (I) which show increased expression in diseased bone and joint
CC tissue e.g. D102 (type 2 Iodothyronine deiodinase); ANK (pyrophosphate
CC transporter); SHOX2 (short stature homeobox 2); TASK4 (potassium ion
CC channel protein); EphA3 (Eph receptor A3); and/or MMP14 (matrix
CC metalloproteinase 16). (A) have antiarthritic, antirheumatic, osteopathic
CC and antiinflammatory activities. (A) can be used for the prevention,
CC treatment and diagnosis of diseases involving the abnormal formation or
CC development of bone and cartilage (such as arthritis deformans), chronic
CC rheumatoid arthritis, synovial inflammation, or localised arthritis (such
CC as tennis elbow). The present sequence represents human EphA3, from the
CC present invention
XX
SQ Sequence 983 AA;
Query Match 55.5%; Score 1799; DB 6; Length 983;
Best Local Similarity 57.0%; Pred. No. 3,5e-148;
Matches 332; Conservative 103; Mismatches 131; Indels 16; Gaps 6;
QY 28 QAAKEVLLDLSKAOQTELEWISSPPSGMEISGLDENYTPRTYQVCYQVMEPNQNNWLT 87
DB 25 QPSENEVNLDSKTIQDELWISYPSHGWIEISGVDEHYTPRTYQVCNWNWLT 84
QY 88 NWSKGAORIFVELKFTLRDNCNLSLPGVLGTCRFTFLYYEENDYDGRNIRENLVKID 147
DB 85 NWPRNSAQKIYELKFTLRDNCNLSLPGVLGTCRFTFLYYEENDYDGRNIRENLVKID 144
QY 148 TIAADESFTQDGERMKLNTVEIREIGPLSKKGFYLAFOVAGACIALVSXYKKYKCKMT 207
DB 145 TIAADESFTQMDGDRILKLNTEIREVGPVNNKGFYLAFOVAGACIALVSXYKKYKCKMT 204
QY 208 IYENLAVFPPTYGSESSLYEVRGTCVSSAEBAENSPPMCHSAGEMLVPIGKICCKA 267
DB 205 IYVNLAMFPDTPV-MDSQSLVEVRGSCVNNKSKE--EDPPRMVCTSTEGEMLVPIGKICCKA 261
QY 268 GYOQKGDTCPCGRFRFYKSSODLQCRPTHSFSDRGSCRCEDDGYFAPSDPPYVA 327
DB 262 GYBERGFMCAQCRPGFYKALDGNMKCAKCPHSHSTQDGSMMNCRCENNYFLADKDPSPMA 321
QY 328 CTRPPSAPOULIFNINQTTVSLWSPPADNGRNDVTYRILCKRCWEQEGCVPCGSNTG 387
DB 322 CTRPPSPRNVISININETSVIDLWSPMDLDTGKRDVTFNILCKCGMNIKQCEPCSPNVR 381
QY 388 YMQOQTGLENNYTVMDLHANATFEVEAVNGVSDLSRQRLFAVSTITGQAAPSOVS 447
DB 382 FLPRQGLTNTVTVDDLHANTYTFEIDAANGVSELSPRQFAVSTITGQAAPSPVL 441
QY 448 GWKERVLORSVOLSMQEPHNGVITEYEIKYKQDERTYSTLTCTKS*TSASINNLKP 507
DB 442 TIKKDRSRNSISLSWQEPHNGIILDYEVKYEKQDERTYSTLTARCTNVTISLKP 501
QY 508 GTVYVFOIRAVTAAGYGNYSPLDVALTEBASGMFEATAVSSQNPVITIAVAVAGTI 567
DB 502 DTIVYFOIRARTAGYGNYSPLDVALTEBASGMFEATAVSSQNPVITIAVAVAGTI 564
QY 568 ILVFMVFGIIGRRHCGYSKADQDEGBELYFHSVLTNHELSV 609
DB 555 LITVIVY-VLIG-RFCGYKSKHGADKRLHF---GNGHLK 590

Search completed: August 23, 2005, 08:32:33
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